

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C07K 14/505, A61K 38/18</b>		A2	(11) International Publication Number: <b>WO 96/40772</b> (43) International Publication Date: 19 December 1996 (19.12.96)
(21) International Application Number: <b>PCT/US96/09469</b>		(81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 6 June 1996 (06.06.96)			
(30) Priority Data: 08/484,135 7 June 1995 (07.06.95) US			
(71) Applicant ( <i>for all designated States except US</i> ): JOHNSON & JOHNSON [US/US]; One Johnson & Johnson Plaza, New Brunswick, NJ 08933-0001 (US).		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(72) Inventors; and (75) Inventors/Applicants ( <i>for US only</i> ): JOHNSON, Dana, L. [US/US]; 1343 Lonely Cottage Road, Upper Black Eddy, PA 18972 (US). ZIVIN, Robert, A. [US/US]; 6 Glenbrook Court, Lawrenceville, NJ 08648 (US).			
(74) Agents: CIAMPORCERO, Audley, A., Jr. et al.; Johnson & Johnson, One Johnson & Johnson Plaza, New Brunswick, NJ 08933-0001 (US).			
(54) Title: AGONIST PEPTIDE DIMERS			
(57) Abstract			
<p>The present invention is directed to the dimerization of agonists and antagonists of cell surface receptors and particularly to peptide dimers which behave as cell surface receptor agonists in their dimeric form. Such receptors belong to the dimerization-mediated activation class often observed among receptors for growth and differentiation factors. The agonists of this class of receptors is understood to effect dimerization of the receptor and thus signal initiation. The present invention exemplifies dimers of erythropoietin (EPO) agonists and antagonists comprising a core amino acid sequence of X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub> (SEQ ID NO: 1) wherein each amino acid is indicated by standard one letter abbreviation; X<sub>3</sub> can be C, A, <math>\alpha</math>-amino-<math>\gamma</math>-bromobutyric acid or Hoc; X<sub>4</sub> can be R, H, L or W; X<sub>5</sub> can be M, F, or I; X<sub>6</sub> is independently selected from any one of the 20 genetically coded L-amino acids or the stereoisomeric D-amino acids; X<sub>7</sub> can be D, E, I, L or V; and X<sub>8</sub> can be C, A, <math>\alpha</math>-amino-<math>\gamma</math>-bromobutyric acid or Hoc, provided that either X<sub>3</sub> or X<sub>8</sub> is C or Hoc.</p>			

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgyzstan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic	KR	Republic of Korea	SE	Sweden
CG	Congo	KZ	Kazakhstan	SG	Singapore
CH	Switzerland	LJ	Liechtenstein	SI	Slovenia
CI	Côte d'Ivoire	LK	Sri Lanka	SK	Slovakia
CM	Cameroon	LR	Liberia	SN	Senegal
CN	China	LT	Lithuania	SZ	Swaziland
CS	Czechoslovakia	LU	Luxembourg	TD	Chad
CZ	Czech Republic	LV	Latvia	TG	Togo
DE	Germany	MC	Monaco	TJ	Tajikistan
DK	Denmark	MD	Republic of Moldova	TT	Trinidad and Tobago
EE	Estonia	MG	Madagascar	UA	Ukraine
ES	Spain	ML	Mali	UG	Uganda
FI	Finland	MN	Mongolia	US	United States of America
FR	France	MR	Mauritania	UZ	Uzbekistan
GA	Gabon			VN	Viet Nam

1

AGONIST PEPTIDE DIMERS5  
10  
15  
20  
25FIELD OF THE INVENTION

The present invention is directed to the dimerization of agonists and antagonists of cell surface receptors and particularly to peptide dimers which behave as cell surface receptor agonists in their dimeric form. Such receptors belong to the dimerization-mediated activation class often observed among receptors for growth and differentiation factors. The agonists of this class of receptors is understood to effect dimerization of the receptor and thus signal initiation. The present invention exemplifies dimers of erythropoietin (EPO) agonists and antagonists comprising a core amino acid sequence of  $X_3X_4X_5GPX_6TWX_7X_8$  (SEQ ID NO: 1) wherein each amino acid is indicated by standard one letter abbreviation;  $X_3$  can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc;  $X_4$  can be R, H, L or W;  $X_5$  can be M, F, or I;  $X_6$  is independently selected from any one of the 20 genetically coded L-amino acids or the stereoisomeric D-amino acids;  $X_7$  can be D, E, I, L or V; and  $X_8$  can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc, provided that either  $X_3$  or  $X_8$  is C or Hoc.

30

BACKGROUND OF THE INVENTION

Erythropoietin (EPO) is a glycoprotein hormone with an approximate molecular weight of 34,000 daltons. The primary role of EPO, which is synthesized in the kidneys of mammals, is to stimulate mitotic cell division and differentiation of erythrocyte precursor cells. As a result, EPO acts to stimulate and to

-2-

1 regulate the production of erythrocytes. Erythrocytes,  
and the hemoglobin contained therein, play a central  
role in supplying oxygen to the body. Thus, the  
5 stimulation of erythrocyte production is able to  
increase the oxygen-carrying capacity of the blood.

10 During normal conditions, EPO is present in  
very low concentrations in plasma. Under hypoxic  
conditions, the amount of EPO in the circulation is  
increased in response to reduced O<sub>2</sub> blood levels.

15 Hypoxia may be caused from various conditions including  
the loss of large amounts of blood, destruction of red  
blood cells by over-exposure to radiation or  
chemotherapeutic agents, reduction in oxygen intake due  
to high altitudes or prolonged unconsciousness, or by  
various forms of anemia. As the hypoxic condition  
diminishes, the amount of EPO produced subsequently  
diminishes.

20 Because of the essential role of EPO in red  
blood cell formation, the hormone is useful in both the  
diagnosis and the treatment of blood disorders  
characterized by low or defective red blood cell  
production. Recent studies provide a basis for the  
efficacy of EPO therapy in a variety of disease states,  
disorders, and states of hematologic irregularity,  
25 including: beta-thalassemia (See, Vedovato et al.  
(1984) Acta. Haematol. 71:211-213); cystic fibrosis  
(See, Vichinsky et al. (1984) J. Pediatric 105:15-21);  
pregnancy and menstrual disorders (See, Cotes et al.  
(1983) Brit. J. Obstet. Gynaecol. 90:304-311); early  
30 anemia of prematurity (See, Haga et al. (1983) Acta  
Pediatr. Scand. 72:827-831); spinal cord injury (See,

-3-

1        Claus-Walker et al. (1984) Arch. Phys. Med. Rehabil.  
65:370-374); space flight (See, Dunn et al. (1984) Eur.  
J. Appl. Physiol.

5        52:178-182); acute blood loss (See,  
Miller et al. (1982) Brit. J. Haematol. 52:545-590);  
aging (See, Udupa et al. (1984) J. Lab. Clin. Med.  
103:574-588); various neoplastic disease states  
accompanied by abnormal erythropoiesis (See, Dainiak et  
al. (1983) Cancer 5:1101-1106); and renal insufficiency  
(See, Eschbach et al. (1987) N. Engl. J. Med. 316:73-78).

10        Although purified, homogenous EPO has been  
characterized, little is known about the mechanism of  
EPO-induced erythroblast proliferation and  
differentiation. The specific interaction of EPO with  
progenitor cells of immature red blood cells, platelets,  
15        and megakaryocytes has not been described. This is due  
in part, to the small number of surface EPO receptor  
molecules on normal erythroblasts and on the  
erythroleukemia cell lines. See Krantz and Goldwasser  
20        (1984) Proc. Natl. Acad. Sci. USA, 81:7574-7578; Branch  
et al. (1987) Blood 69:1782-1785; Mayeux et al. (1987)  
FEBS Letters 211:229-233; Mufson and Gesner (1987) Blood  
69:1485-1490; Sakaguchi et al. (1987) Biochem. Biophys.  
Res. Commun. 146:7-12; Sawyer et al. (1987) Proc. Natl.  
Acad. Sci. USA 84:3690-3694; Sawyer et al. (1987) J.  
Biol. Chem. 262:5554-5562; and Todokoro et al. (1988)  
Proc. Natl. Acad. Sci. USA 84:4126-4130. The DNA  
25        sequences and encoded peptide sequences for murine and  
human EPO receptor proteins have been described. See,  
D'Andrea et al. PCT Patent Publication No. WO 90/08822  
30        (published 1990).

- 4 -

1       The EPO-receptor (EPO-R) belongs to the class  
of growth-factor-type receptors which are activated by a  
ligand-induced protein dimerization. Other hormones and  
5       cytokines such as human growth hormone (hGH),  
granulocyte colony stimulating factor (G-CSF), epidermal  
growth factor (EGF) and insulin can cross-link two  
receptors resulting in juxtaposition of two cytoplasmic  
tails. Many of these dimerization-activated receptors  
have protein kinase domains within the cytoplasmic tails  
10      that phosphorylate the neighboring tail upon  
dimerization. While some cytoplasmic tails lack  
intrinsic kinase activity, these function by association  
with protein kinases. The EPO receptor is of the latter  
type. In each case, phosphorylation results in the  
15      activation of a signaling pathway.

In accordance with the present invention, it  
has been discovered that the dimerization of peptide  
agonists and antagonists of dimerization-mediated  
receptors, such as EPO-R, increase the biological  
20      efficacy relative to the biological activity of the  
'monomeric' agonists and alters the properties of the  
antagonists such that, these dimers function as  
agonists, exhibiting biological activity.

25      SUMMARY OF THE INVENTION

In a first embodiment, the present invention  
is directed to peptide dimers which behave as cell-  
surface receptor agonists, dimers which exhibit binding  
and signal initiation of growth factor-type receptors.  
30      In one embodiment, the present invention provides  
peptide dimers which behave as EPO agonists. These

-5-

1 dimers have two 'monomeric' peptide units of 10 to 40 or  
more amino acids, preferably 14 to about 20 residues in  
length, comprising a core amino acid sequence of  
5  $X_1X_2X_3GPX_6TWX_7X_8$  (SEQ ID NO: 1) where each amino acid is  
indicated by standard one letter abbreviation;  $X_3$  can be  
 $C$ ,  $A$ ,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or  $Hoc$ , where  $Hoc$  is  
homocysteine;  $X_4$  can be  $R$ ,  $H$ ,  $L$ , or  $W$ ;  $X_5$  can be  $M$ ,  $F$ ,  
or  $I$ ;  $X_6$  is independently selected from any one of the  
10 20 genetically coded L-amino acids or the stereoisomeric  
D-amino acids;  $X_7$  can be  $D$ ,  $E$ ,  $I$ ,  $L$ , or  $V$ ; and  $X_8$  can be  
 $C$ ,  $A$ ,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or  $Hoc$ , where  $Hoc$  is  
homocysteine, provided that either  $X_3$  or  $X_8$  is  $C$  or  $Hoc$ .  
Preferably, the monomeric peptide unit of the dimer  
comprises a core sequence  $YX_2X_3X_4X_5GPX_6TWX_7X_8$  (SEQ ID  
15 NO: 2) where each amino acid is indicated by standard  
one letter abbreviation; each  $X_2$  and  $X_6$  is independently  
selected from any one of the 20 genetically coded L-  
amino acids;  $X_3$  can be  $C$ ,  $A$ ,  $\alpha$ -amino- $\gamma$ -bromobutyric  
acid, or  $Hoc$ , where  $Hoc$  is homocysteine;  $X_4$  can be  $R$ ,  $H$ ,  
20  $L$ , or  $W$ ;  $X_5$  can be  $M$ ,  $F$ , or  $I$ ;  $X_7$  can be  $D$ ,  $E$ ,  $I$ ,  $L$ , or  
 $V$ ; and  $X_8$  can be  $C$ ,  $A$ ,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or  
 $Hoc$ , where  $Hoc$  is homocysteine, provided that either  $X_3$   
or  $X_8$  is  $C$  or  $Hoc$ .

25 More preferably, the monomeric peptide unit of  
the dimer comprises a core sequence of amino acids  
 $X_1YX_2X_3X_4X_5GPX_6TWX_7X_8X_9X_{10}X_{11}$  (SEQ ID NO: 3), where each  
amino acid is indicated by standard one letter  
abbreviation; each  $X_1$ ,  $X_2$ ,  $X_6$ ,  $X_7$ ,  $X_9$ ,  $X_{10}$ , and  $X_{11}$  is  
independently selected from any one of the 20  
30 genetically coded L-amino acids;  $X_3$  can be  $C$ ,  $A$ ,  $\alpha$ -  
amino- $\gamma$ -bromobutyric acid, or  $Hoc$ , where  $Hoc$  is

-6-

1 homocysteine; X<sub>4</sub> can be R, H, L, or W; X<sub>5</sub> can be M, F, or I; X<sub>7</sub> can be D, E, I, L or V; and X<sub>8</sub> can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or Hoc, where Hoc is homocysteine, provided that either X<sub>3</sub> or X<sub>8</sub> is C or Hoc.

5 In a more preferred embodiment, both X<sub>3</sub> and X<sub>8</sub> are C and thus, the monomeric peptide unit of the dimer comprises a core sequence of amino acids

10 X<sub>1</sub>YX<sub>2</sub>CX<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>CX<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 4). More preferably, the monomeric peptide unit comprises a core sequence of amino acids X<sub>1</sub>YX<sub>2</sub>CX<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>CX<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 5), where X<sub>4</sub> can be R or H; X<sub>5</sub> can be F or M; X<sub>6</sub> can be I, L, T, M, or V; X<sub>7</sub> is D or V; X<sub>9</sub> can be G, K, L, Q, R, S, or T; and X<sub>10</sub> can be A, G, P, R, or Y. In a most preferred embodiment, the monomeric peptide unit of 15 the dimer will comprise a core sequence of amino acids X<sub>1</sub>YX<sub>2</sub>CX<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>CX<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 6), where X<sub>1</sub> can be D, E, L, N, S, T, or V; X<sub>2</sub> can be A, H, K, L, M, S, or T; X<sub>4</sub> is R or H; X<sub>5</sub> can be K, R, S, or T; and X<sub>10</sub> is P. Particularly preferred monomeric peptide units of 20 the dimers include:

GGLYLCRFGPVTVDCGYKGG (SEQ ID NO: 7);  
GGTYSCHFGPLTWVCKPQGG (SEQ ID NO: 8);  
GGDYHCRMGPLTWVCKPLGG (SEQ ID NO: 9);  
VGNYMCHFGPITWVCRPGGG (SEQ ID NO: 10);  
GGVYACRMGPITWVCSPLGG (SEQ ID NO: 11);  
VGNYMAHMGPIIWVCRPGG (SEQ ID NO: 12);  
GGTYSCHFGPLTWVCKPQ (SEQ ID NO: 13);  
GGLYACHMGPMTWVCQPLRG (SEQ ID NO: 14);  
TIAQYICYMGPETWECRPSPKA (SEQ ID NO: 15);  
YSCHFGPLTWVCK (SEQ ID NO: 15);  
YCHFGPLTWVC (SEQ ID NO: 17); and

-7-

1

SCHFGPLTWVCK

(SEQ ID NO: 18).

Other particularly preferred monomeric peptide units of the present dimers include peptides comprising a core sequence of the formula  $(AX_2)_nX_3X_4X_5GPX_6TWX_7X_8$  (SEQ ID NO: 19) wherein  $X_2$  through  $X_8$  are as previously defined herein (SEQ ID NO: 2),  $n$  is 1 or 0 and A is any one of the naturally occurring L-amino acids except Y (tyrosine);  $n$  is defined herein as the number of occurrences of  $(AX_2)$  which can be 1 or none in the core sequence. When  $(AX_2)$  is present, i.e. when  $n = 1$ , A is not tyrosine and A is not any non-naturally occurring aromatic amino acid analog. Such monomeric peptide units of the dimers of this invention can be prepared by truncating the peptides of Fig. 9, for example, from the N-terminus to delete the Y, tyrosine residue in SEQ ID NOS. 21 - 93. Such monomeric peptides can also be prepared by substitution of Y in position A in the peptides of Fig. 9.

20

In accordance with the present invention the monomeric units of the dimers can be the same or different.

25

In a preferred embodiment polyethylene glycol (PEG) is employed as a linker to form the dimeric peptides of the present invention through a covalent bond.

30

In another embodiment, the present invention is directed to pharmaceutical compositions comprising at least one dimer peptide of the invention and a pharmaceutical carrier.

-8-

1

In a further embodiment, the present invention provides a method for therapeutically treating a mammal having a condition resulting from a hormone or growth factor deficiency by administration of at least one of the dimer peptides of the present invention.

5

In a still further embodiment, a method for therapeutically treating a mammal having a condition resulting from a deficiency of EPO or from reduced levels of blood oxygen caused by a decrease in erythrocyte number is provided.

10

In another embodiment of this invention, a method is provided for preparing agonists of cell-surface receptors wherein agonists of the class of cell-surface or dimerization-mediated receptors are dimerized to enhance the in vitro or in vivo biological activity of the cell-surface receptor relative to the monomeric agonists from which the dimer is derived. This method is also directed to the preparation of agonists of such growth-factor-type receptors by dimerizing antagonists of these receptors; the dimerized 'antagonists' thereby exhibit agonist biological activity in vitro and in vivo. In a preferred embodiment, the present method is directed to the preparation of EPO-R dimer agonists from monomeric EPO-R antagonists.

15

#### BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows a major peak, with a retention time of 37 minutes, of the dimerized EPO peptide, GGTYSCHFGPLTWVCKPQGG (SEQ ID NO: 8)

20

25

-9-

1

Fig. 2 shows a major peak, with a retention time of 48 minutes, following purification of the dimerized EPO peptide, (SEQ ID NO: 8).

5

Fig. 3 depicts the MALDI-TOF mass spectral analysis of the dimerized peptides, including peptide (SEQ ID NO: 8), GGTYSCHFGPLTWVCKPQ (SEQ ID NO: 13) and SCHFGGPLTWVCK (SEQ ID NO: 18).

10

Fig. 4 shows the SDS-PAGE analysis of DPDPB crosslinking of EPO binding protein (EBP) in the presence and absence of EPO agonist peptides.

15

Fig. 5 demonstrates equilibrium EPO binding to immobilized EPO binding protein. Panel A represents the equilibrium binding data and Panel B (inset) is the linear transformation (Scatchard) of the data set in Panel A.

20

Fig. 6 depicts the results of a competitive binding assay run on the EPO agonist peptide (SEQ ID NO: 8) in competitive binding with [<sup>125</sup>I]EPO to EBP beads (Panel A); and EPO responsive cell proliferation studies in FDC-P1 derived cell lines containing either a human (Panel B) or murine EPO receptor (Panel C).

25

Fig. 7 is a graphic representation of the results of the exhypoxic mouse bioassay; stimulation of the incorporation of [<sup>59</sup>Fe] into nascent red blood cells by EPO, peptide (SEQ ID NO: 8) (Panel A) and peptide (SEQ ID NO: 8) dimer (Panel B).

30

Fig. 8 demonstrates the effect of PEG dimerization of peptide (SEQ ID NO: 18) activity in EPO responsive cell proliferation studies in FDC-P1 derived cell lines containing a human EPO receptor.

-10-

1

Fig. 9 provides the sequences of representative monomeric peptides of the present invention.

5

DETAILED DESCRIPTION OF THE INVENTION

10

The present invention is directed to peptide dimers which behave as cell surface receptor agonists, dimers which exhibit binding and signal initiation of growth-factor-type receptors. Sometimes called cell-surface receptors, growth-factor-type receptors or dimerization-mediated activator-receptors, these are a class of molecules which are understood to be activated by ligand-induced or ligand stabilized dimerization.

15

Agonists of such receptors typically include large polypeptide hormones including the cytokines, insulin and various other growth or differentiation factors.

20

The agonists are understood to induce dimerization of the receptor and thereby effect signal initiation. Such agonists are believed to effectively cross-link two receptors resulting in the repositioning of cytoplasmic tails which may directly or indirectly effect phosphorylation of the cytoplasmic tails and activation of a signaling pathway.

25

The present invention specifically includes those molecules which behave as agonists of cell-surface receptors when dimerized in accordance with this invention. Such dimer agonists can include 'monomeric' units which exhibit agonist or antagonist activity for the related receptor molecule and may be the same or different. The dimers are preferably peptides but may alternatively be small molecule pharmacophores. These molecules when dimerized exhibit agonist activity of

30

35

-11-

1      cell-surface receptors in vitro and in vivo. Such  
receptors include, for example, EPO, GM-CSF, G-CSF, M-  
CSF, GH, EGF, PDGF, VEGF, Insulin and FGF. Other  
5      receptors which are activated by heterodimerization or  
multimerization may also be subject to activation by  
this mechanism including, IL-3, IL-5, IL-6, IL-2 and  
TPO. The dimers of the present invention have two  
10     'monomeric' peptide units of 10 to 40 or more amino  
acids, preferably 14 to about 20 amino acid residues in  
length. In a preferred embodiment, these monomeric  
peptide units comprise a core sequence of amino acids  
X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub> (SEQ ID NO: 1) where each amino acid is  
indicated by standard one letter abbreviation; X<sub>3</sub> can be  
15     C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or Hoc, where Hoc is  
homocysteine; X<sub>4</sub> can be R, H, L, or W; X<sub>5</sub> can be M, F,  
or I; X<sub>6</sub> is independently selected from any one of the  
20     20 genetically coded L-amino acids or the stereoisomeric  
D-amino acids; X<sub>7</sub> can be D, E, I, L, or V; and X<sub>8</sub> can be  
C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or Hoc, where Hoc is  
homocysteine, provided that either X<sub>3</sub> or X<sub>8</sub> is C or Hoc.  
20     Preferably, the monomeric peptide unit of the dimer  
comprises a core sequence YX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub> (SEQ ID  
NO: 2) where each amino acid is indicated by standard  
one letter abbreviation; each X<sub>2</sub> and X<sub>8</sub> is independently  
25     selected from any one of the 20 genetically coded L-  
amino acids; X<sub>3</sub> can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric  
acid, or Hoc, where Hoc is homocysteine; X<sub>4</sub> can be R, H,  
L, or W; X<sub>5</sub> can be M, F, or I; X<sub>7</sub> can be D, E, I, L, or  
V; and X<sub>8</sub> can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or  
30     Hoc, where Hoc is homocysteine, provided that either X<sub>3</sub>  
or X<sub>8</sub> is C or Hoc.

-12-

1

More preferably, the monomeric peptide unit of the dimer comprises a core sequence of amino acids  $X_1YX_2X_3X_4X_5GPX_6TWX,X_6X_9X_{10}X_{11}$  (SEQ ID NO: 3), where each amino acid is indicated by standard one letter abbreviation; each  $X_1$ ,  $X_2$ ,  $X_6$ ,  $X_9$ ,  $X_{10}$ , and  $X_{11}$  is independently selected from any one of the 20 genetically coded L-amino acids;  $X_3$  can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or Hoc, where Hoc is homocysteine;  $X_4$  can be R, H, L, or W;  $X_5$  can be M, F, or I;  $X_9$  can be D, E, I, L or V; and  $X_{10}$  can be C, A,  $\alpha$ -amino- $\gamma$ -bromobutyric acid, or Hoc, where Hoc is homocysteine, provided that either  $X_3$  or  $X_6$  is C or Hoc.

10

In a more preferred embodiment, both  $X_3$  and  $X_6$  will be C and thus, the monomeric peptide unit of the dimer comprises a core sequence of amino acids

15

$X_1YX_2CX_4X_5GPX_6TWX,CX_9X_{10}X_{11}$  (SEQ ID NO: 4). More preferably, the monomeric peptide unit comprises a core sequence of amino acids  $X_1YX_2CX_4X_5GPX_6TWX,CX_9X_{10}X_{11}$  (SEQ ID NO: 5), where  $X_4$  can be R or H;  $X_5$  can be F or M;  $X_6$  can be I, L, T, M, or V;  $X_9$  is D or V;  $X_{10}$  can be G, K, L, Q, R, S, or T; and  $X_{11}$  can be A, G, P, R, or Y. In a most preferred embodiment, the monomeric peptide unit of the dimer comprises a core sequence of amino acids  $X_1YX_2CX_4X_5GPX_6TWX,CX_9X_{10}X_{11}$  (SEQ ID NO: 6), where  $X_1$  can be D, E, L, N, S, T, or V;  $X_2$  can be A, H, K, L, M, S, or T;  $X_4$  is R or H;  $X_5$  can be K, R, S, or T; and  $X_{10}$  is P. Particularly preferred monomeric peptide units of the present dimers include:

20

25

30

GGLYLCRFGPVTWDCGYKGG (SEQ ID NO: 7);

GGTYSCHFGPLTWVCKPQGG (SEQ ID NO: 8);

35

-13-

1 GGDYHCRMGPLTWVCKPLGG (SEQ ID NO: 9);  
VGNYMCHFGPITWVCRPGGG (SEQ ID NO: 10);  
GGVYACRMGPITWVCSPLGG (SEQ ID NO: 11);  
5 VGNYMAHMGPITWVCRPGG (SEQ ID NO: 12);  
GGTYSCHFGPLTWVCKPQ (SEQ ID NO: 13);  
GGLYACHMGPMTWVCQPLRG (SEQ ID NO: 14);  
TIAQYICYMGPETWECRPSPKA (SEQ ID NO: 15);  
10 YSCHFGPLTWVCK (SEQ ID NO: 16);  
YCHFGPLTWVC (SEQ ID NO: 17); and  
SCHFGPLTWCK (SEQ ID NO: 18).

The dimer peptides of the present invention exhibit increased biological potency in vitro and in vivo relative to the monomeric agonists from which the dimers are derived. Moreover, cell surface receptor antagonists can be 'converted' to cell surface receptor agonists in accordance with the present invention. Specifically, a cell surface receptor antagonist can be dimerized with PEG or another appropriate linker which permits mutual binding of the monomeric moieties with the receptors. As a result, the dimer exhibits effective binding to the target receptor and behaves as an agonist. Accordingly, the dimers of this invention demonstrate enhanced biological potency in vitro and in vivo relative to their monomeric forms.

The dimer peptides of the present invention bind to and biologically activate the cell surface receptor or otherwise behave as agonists and are preferably formed by employing polyethylene glycol as a linker between the monomeric peptide units described herein. While other conventional chemical systems can

-14-

1 also be employed to form the dimer peptides of this  
invention including using other known polymeric  
compounds, pegylation is preferred.

5 The linking compounds of the present invention  
include any molecule which covalently binds the  
monomeric peptides at an appropriate distance or which  
otherwise effects dimerization of the particular cell  
surface receptor thereby initiating biological efficacy.

10 Starting with an appropriate synthetic  
peptide, containing a free amino group or other reactive  
site such as hydroxyls, carboxylic acids or sulfhydryls,  
the peptide is added in excess to a reaction mixture  
containing a corresponding reactive polymer. The  
polymer can be of a repeating nature such as  
15 polyethylene glycol, peptides, modified peptides or  
peptide analogs. Alternatively, the peptide can be  
dimerized on a small molecule scaffold such as activated  
benodiazepins, oxazolones, azalactones, aminimides or  
diketopiperazines. The most readily available linker of  
20 variable distance are ones based on linear unbranched  
polyethylene glycols.

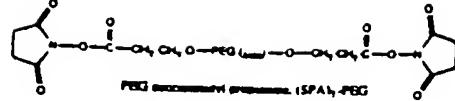
25 The following is a schematic of a preferred  
preparatory methodology employing PEG succinimidyl  
propionate as the linker between the monomer units of  
the dimer peptides.

30

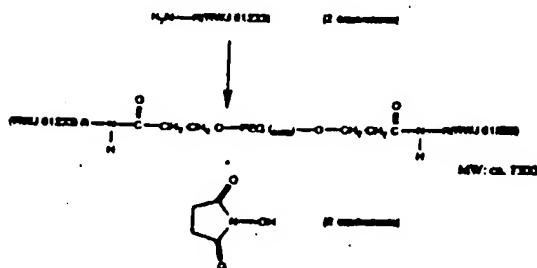
35

-15-

1



5



10

Dimerization and especially pegylation in a head-to-head (amino to amino terminus) or head-to-tail (amino to carboxyl terminus) configuration is preferred relative to internal covalent binding of the monomeric peptides. The 'monomer' units of the dimer peptides of the present invention can be the same or different, although the same are preferred.

The monomeric peptides which are used to form the dimers of the present invention can be prepared by classical chemical methods well known in the art. The standard methods include, for example, exclusive solid phase synthesis and recombinant DNA technology. See, e.g. Merrifield (1963) J. Am. Chem. Soc. 85:2149. Solid phase synthesis is typically commenced from the C-terminal end of the peptide using an  $\alpha$ -amino protected resin. A suitable starting material can be prepared by attaching the required  $\alpha$ -amino acid to a chloromethylated resin (such as BIO-BEADS SX-1, Bio Rad Laboratories, Richmond, CA), a hydroxymethyl resin, (described by Bodanszky et al. (1966) Chem. Ind.

- 16 -

1

(London) 38:1597) or a benzhydrylamine resin (described by Pietta and Marshall (1970) Chem. Commun. 650).

5

The  $\alpha$ -amino protecting groups are those known to be useful in the art of stepwise synthesis or peptides. Included are acyl type protecting groups (e.g. formyl, trifluoroacetyl, acetyl), aromatic urethane type protecting groups (e.g. benzyloxycarboyl (Cbz) and substituted Cbz), aliphatic urethane protecting groups (e.g., t-butyloxycarbonyl (Boc), isopropylloxycarbonyl, cyclohexyloxycarbonyl) and alkyl type protecting groups (e.g., benzyl and triphenylmethyl). The preferred X-amino protecting group is Fmoc. The side chain protecting group (typically ethers, esters, trityl, PMC, and the like) remains intact during coupling and is not split off during the deprotection of the amino-terminus protecting group or during coupling. The side chain protecting group must be removable upon the completion of the synthesis of the final peptide and under reaction conditions that will not alter the target peptide.

10

15

20

25

30

The side chain protecting groups for Tyr include tetrahydropyranyl, tert-butyl, trityl, benzyl, Cbz, Z-Br-Cbz, and 2,5-dichlorobenzyl. The side chain protecting groups for Asp include benzyl, 2,6-dichlorobenzyl, methyl, ethyl, and cyclohexyl. The side chain protecting groups for Thr and Ser include acetyl, benzoyl, trityl, tetrahydropyranyl, benzyl, 2,6-dichlorobenzyl, and Cbz. The side chain protecting groups for Thr and Ser are benzyl. The side chain protecting groups for Arg include nitro, Tosy. (Tcs), Cbz, adamantlyloxycarbonyl mesitoylsulfonyl (Mts), or

-17-

1. Boc. The side chain protecting groups for Lys include Cbz, 2-chlorobenzylloxycarbonyl (2-Cl-Cbz), 2-bromobenzylloxycarbonyl (2-BrCbz), Tos, or Boc.

5 After removal of the  $\alpha$ -amino protecting group, the remaining protected amino acids are coupled stepwise in the desired order. Each protected amino acid is generally reacted in about a 3-fold excess using an appropriate carboxyl group activator such as 2-(1H-benzo[d]imidazol-1-yl)-1,1,3,3tetramethyluronium  
10 hexafluorophosphate (HBTU) or dicyclohexylcarbodiimide (DCC) in solution of methylene chloride ( $\text{CH}_2\text{Cl}_2$ ), or dimethyl formamide (DMF) mixtures.

15 After the desired amino acid sequence has been completed, the desired peptide is decoupled from the resin support by treating the mixture with a reagent such as trifluoroacetic acid (TFA) or hydrogen fluoride (HF). These reagents not only cleave the peptide from the resin, but also cleave all remaining side chain protecting groups. When the chloromethylated resin is used, hydrogen fluoride treatment results in the formation of the free peptide acids. When the benzhydrylamine resin is used, hydrogen fluoride treatment results directly in the free peptide amide.  
20 Alternatively, when the chloromethylated resin is employed, the side chain protected peptide can be decoupled by treatment of the peptide resin with ammonia to give the desired side chain protected amide or with an alkylamine to give a side chain protected alkylamide or dialkylamide. Side chain protection is then removed in the usual fashion by treatment with hydrogen fluoride to give the free amides, alkylamides, or dialkylamides.

-18-

1.

These procedures can also be used to synthesize peptides in which amino acids other than the 20 naturally occurring, genetically encoded amino acids are substituted at one, two or more positions of any of 5 the compounds of the invention. For instance, naphthylalanine can be substituted for tryptophan, facilitating synthesis. Other synthetic amino acids that can be substituted into the peptides of the present 10 invention include L-hydroxypropyl, L-3, 4-dehydroxyphenylalanyl,  $\delta$  amino acids such as L- $\delta$ -hydroxylysyl and D- $\delta$ -methylalanyl, L- $\alpha$ -methylalanyl,  $\beta$  amino acids, and isoquinolyl. D-amino acids and non-naturally occurring synthetic amino acids can also be 15 incorporated into the peptides of the present invention.

15

In another embodiment of the present invention, a method of enhancing the in vitro or in vivo biological potency of a cell surface receptor agonist is provided. This methodology is achieved by dimerizing the receptor agonist with a linker molecule, such as 20 PEG, to form an appropriate spatial relationship between the monomeric peptide units of the dimer and thereby permitting each of the constituents of the dimers to bind to their receptors to achieve enhanced biological potency, i.e., to dimerize and thereby activate the 25 receptors to induce the relevant biological activity of the particular cell-surface receptor, e.g. EPO-R. Biological activity can be measured by the skilled artisan in various in vitro and in vivo assays and as demonstrated in the examples of the present invention.

30

The peptide or molecule with binding affinity for a given receptor will have increased conformational

-19-

1 flexibility leading to fewer barriers to effective  
receptor interaction and subsequently receptor  
activation. This is also indicated for molecules which  
5 can bind but not activate a receptor subtype in that  
such molecules can become more effective inhibitors of  
ligand binding.

The present invention further provides a  
method for altering a cell-surface receptor antagonist,  
10 a molecule exhibiting receptor binding but no biological  
activity, to behave as a cell-surface receptor agonist  
in vitro or in vivo. This method is achieved by  
dimerizing the antagonist molecule with an appropriate  
15 linker molecule such as PEG, other polymerized molecules  
or a peptide. In a preferred embodiment, an EPO  
antagonist, i.e. a peptide exhibiting receptor binding  
but no biological EPO activity can be altered by  
dimerization to obtain a dimer which behaves as an EPO  
20 receptor agonist. Thus, for example, in the case of  
EPO-R these include the monomeric peptide units of the  
present dimers comprising a core sequence of general  
formula  $(AX_2)_nX_3X_4X_5GPX_6TWX_7X_8$  (SEQ ID NO: 19) wherein  
25  $X_2$  through  $X_8$  are as previously defined herein, in (SEQ  
ID NO: 2), n is 1 or 0 and A is any one of the naturally  
occurring L-amino acids except Y (tyrosine); n is  
defined herein as the number of occurrences of  $(AX_2)$   
which can be 1 or none in the core sequence. When  $X_2$  is  
30 present, i.e., when n = 1, A is not tyrosine and A is  
not any non-naturally occurring aromatic amino acid  
analog. Such monomeric peptide units of the dimers of  
this invention can be prepared by truncating the  
peptides of Fig. 9, for example, from the N-terminus to

-20-

1 delete the Y, tyrosine residue in SEQ ID NOS. 21 - 93.  
Such monomeric peptides can also be prepared by  
substitution of Y in the peptides of Fig. 9.

5 These molecules, demonstrate only binding  
activity in their 'monomeric' form, but exhibit agonist  
activity after dimerization with a linking compound such  
as PEG. Accordingly, the present method comprises  
identifying a monomeric peptide as herein defined which  
does not demonstrate biological activity and dimerizing  
10 that antagonist in accordance with the present invention  
to obtain a cell-surface-receptor agonist i.e., in  
dimeric form. Contacting the appropriate cell-surface  
receptor with the thus formed dimer activates, i.e.  
15 dimerizes such receptors and thus induces biological  
activity of the receptor. Such monomeric units as  
shown in Fig. 9 can be truncated from the N-terminus  
such as SCHFGPLTWVCK (SEQ ID NO: 18) to eliminate the  
tyrosine residue at position A of the formula  
20  $(AX_2)_nX_3X_4X_5GPX_6TWX_7X_8$  (SEQ ID NO: 19) or merely  
substituted with any of the remaining 19 naturally  
occurring amino acids or with other than a non-naturally  
occurring aromatic amino acid analog. In accordance  
with the present invention it has been determined that  
25 the tyrosine residue at position A of the foregoing  
formula is critical to biological activity of the  
monomer peptide. Deletion or substitution of the  
tyrosine eliminates biological activity. When dimerized  
however the entity exhibits enhanced biological  
activity.

30 For example, tyrosine (Y) substituted in the  
formula  $YX_2X_3X_4X_5GPX_6X_8$  (SEQ ID NO: 2) by p-

-21-

1       iodohydroxyphenylalanine, p-fluorohydroxyphenylalanine,  
p-amino-hydroxyphenylalanine act as EPO-R monomer  
agonists but substitution with threonine or alanine for  
5       tyrosine at position Y causes the monomer peptide to act  
as an EPO-R antagonist. However, when dimerized in  
accordance with the present invention, such dimers  
behave as EPO-R agonists. The monomeric peptide units  
identified at Fig. 9, for example, behave as EPO-R  
antagonists in the absence of tyrosine at position Y of  
10      the formula above. When such antagonists are dimerized,  
the dimer behaves as an EPO-R agonist.

15       In a further embodiment of the present  
invention, pharmaceutical compositions comprising at  
least one of the dimers of this invention can be  
employed to therapeutically treat disorders resulting  
from deficiencies of biological factors such as EPO, GH,  
GM-CSF, G-CSF, EGF, PDGF, VEGF, insulin, FGF and the  
like. These pharmaceutical compositions may contain  
20      buffers, salts and other excipients to stabilize the  
composition or assist in the delivery of the dimerized  
molecules.

25       In a preferred embodiment, the present  
invention provides a method for treating disorders  
associated with a deficiency of EPO. The method is  
accomplished by administering at least one of the dimers  
identified herein for a time and under conditions  
sufficient to alleviate the symptoms of the disorder,  
i.e. sufficient to effect dimerization or biological  
activation of EPO receptors. In the case of EPO such  
30      methodology is useful in the treatment of end-stage  
renal failure/dialysis; anemia, especially associated

-22-

1 with AIDS or chronic inflammatory diseases such as  
rheumatoid arthritis and chronic bowel inflammation;  
auto-immune disease; and for boosting the red blood cell  
count of patient when necessary, e.g. prior to surgery  
5 or as pretreatment to transfusion. The dimers of the  
present invention which behave as EPO agonists can be  
used to activate megakaryocytes.

10 Since EPO has been shown to have a mitogenic  
and chemotactic effect on vascular endothelial cells as  
well as an effect on central cholinergic neurons (see,  
e.g., Amagnostou et al. (1990) Proc. Natl. Acad. Sci.  
USA 87:597805982 and Konishi et al. (1993) Brain Res.  
609:29-35), the compounds of this invention can also be  
15 used to treat a variety of vascular disorders, such as  
promoting wound healing, growth of collateral coronary  
blood vessels (such as those that may occur after  
myocardial infarction), trauma, and post vascular graft  
treatment, and a variety of neurological disorders,  
generally characterized by low absolute levels of acetyl  
20 choline or low relative levels of acetyl choline as  
compared to other neuroactive substances e.g.,  
neurotransmitters.

25 Accordingly, the present invention includes  
pharmaceutical compositions comprising, as an active  
ingredient, at least one of the peptide dimers of the  
present invention in association with a pharmaceutical  
carrier or diluent. The dimers of this invention can be  
administered by oral, parenteral (intramuscular,  
30 intraperitoneal, intravenous (IV) or subcutaneous  
injection), transdermal (either passively or using  
iontophoresis or electroporation) or transmucosal

-23-

1 (nasal, vaginal, rectal, or sublingual) routes of administration in dosage forms appropriate for each route of administration.

5 Solid dosage forms for oral administration include capsules, tablets, pill, powders, and granules. In such solid dosage forms, the active compound is admixed with at least one inert pharmaceutically acceptable carrier such as sucrose, lactose, or starch. Such dosage forms can also comprise, as it normal practice, additional substances other than inert diluents, e.g., lubricating, agents such as magnesium stearate. In the case of capsules, tablets and pills, the dosage forms may also comprise buffering, agents. Tablets and pills can additionally be prepared with enteric coatings.

10 Liquid dosage forms for oral administration include pharmaceutically acceptable emulsions, solutions, suspensions, syrups, with the elixirs containing inert diluents commonly used in the art, such as water. Besides such inert diluents, compositions can also include adjuvants, such as wetting agents, emulsifying and suspending agents, and sweetening, flavoring and perfuming agents.

15 Preparations according to this invention for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, or emulsions. Examples of non-aqueous solvents or vehicles are propylene glycol, polyethylene glycol, vegetable oils, such as olive oil and corn oil, gelatin, and injectable organic esters such as ethyl oleate. Such dosage forms may also contain adjuvants such as preserving, wetting,

-24-

1 emulsifying, and dispersing agents. They may be  
sterilized by, for example, filtration through a  
bacteria retaining filter, by incorporating sterilizing  
agents into the compositions, by irradiating the  
5 compositions, or by heating the compositions. They can  
also be manufactured using sterile water, or some other  
sterile injectable medium, immediately before use.

10 Compositions for rectal or vaginal  
administration are preferably suppositories which may  
contain, in addition to the active substance, excipients  
such as cocoa butter or a suppository wax. Compositions  
for nasal or sublingual administration are also prepared  
with standard excipients well known in the art.

15 The dosage of active ingredient in the  
compositions of this invention may be varied; however,  
it is necessary that the amount of the active ingredient  
shall be such that a suitable dosage form is obtained.  
The selected dosage depends upon the desired therapeutic  
20 effect, on the route of administration, and on the  
duration of the treatment desired. Generally dosage  
levels of between 0.001 to 10 mg/kg of body weight daily  
are administered to mammals.

25 As can be appreciated from the disclosure  
above, the present invention has a wide variety of  
applications. Accordingly, the following examples are  
offered by way of illustration, not by way of  
limitation.

30

35

-25-

1

EXAMPLE 1

SDS-PAGE gels (10-20% gradient SDS-PAGE plates, 84 x 70 x 1.0 mm, Integrated Separation Systems, Natick, MA) were stained with Coomassie Brilliant Blue R-250 (BioRad). A commercial preparation of activated difunctional polyethylene glycol (PEG-succinimidyl-propionate, SPA2, MW ca. 3400) was purchased from Shearwater Polymers, Huntsville, AL as was the monofunctional reagent, methoxy-PEG-succinimidyl-propionate, MW ca 5000. Peptide (SEQ ID NO: 8) and all other peptides were obtained from the Peptide Synthesis Facility RWJ-PRI, La Jolla, CA or Quality Controlled Biochemical, Hopkinton MA. These peptides were cyclized via oxidation of their intramolecular cysteines, amidated at the C-terminus and mass confirmed by FAB-MS. All were Ellman Reaction negative. Tris base was obtained from BioRad, Hercules, CA. (DPDPB) and trifluoracetic acid (HPLC grade) were obtained from Pierce Chemical Co., Rockford IL.

20

Mono-PEG conjugation of peptide GGTYSCHFGPLTWVCKPQGG

(SEQ ID NO: 8)

25

This example describes the preparation of mono-PEG conjugates of peptide (SEQ ID NO: 8), using the monofunctional amine reactive polymer analog m-SPA-PEG to be used as a control in experiments described herein. The reaction was carried out with polymer in excess (ca. 3 fold) by resuspending 142.5 mg (0.0286 mmol, MW ca. 5000) of polymer in 4 ml PBS at pH 7.5 and adding 20 mg peptide (SEQ ID NO: 8) (0.0095 mmol, MW 2092) dissolved

35

-26-

1       in 1 ml of 0.1% trifluoroacetic acid. The mixture was  
incubated on ice for 20 hours. The reaction was  
subsequently adjusted to a final concentration 50 mM  
5       Tris by the addition of 1 M tris-HCl at pH 7.5. The  
reaction mixture was incubated on ice for one hour.  
Analytical HPLC suggested that there were two main  
reaction products of essentially equivalent magnitude  
which were not baseline resolved. Preparative HPLC  
10      (using the flatter gradient system described in Example  
8) and conservative cuts resulted in collection of two  
product peaks eluting at ca 44 and 47 minutes. After  
lyophilization, 24.8 mg, 16.5 mg of each species was  
recovered, respectively. Mass spectral analysis of  
these two species demonstrated centroid masses of 7092  
15      (peak 1) and 12036 (peak 2) indicating the coupling of  
one or two PEG molecules, respectively, to the peptide  
(Table I).

20       Tris inactivated polymer. Tris inactivated  
polymer was formed by incubation of 5 mM SPA2 polymer  
dissolved in PBS (Gibco, Gaithersburg, MD) with 50 mM  
tris-HCl, pH 7.5 added and used without further  
purification.

25

30

35

-27-

**TABLE 1**  
**Recovery Yield of Peptide Conjugation Reaction and Apparent Molecular Mass of Product**

I.D. No.	Sequence	Mass	Conjugation Reagent	Main Product Mass (centroid m/z)	Yield (% of theoretical)
8	GGTYSCHFGPLTWCKPKQG	2092	SPA2-PEG (MW ca. 3400)	7834	69
13	GGTYSCHFGPLTWCKPKQ	1978	m-SPA-PEG (MW ca. 5000)	7092 (peak 1) 12036 (peak 2)	-
20	Ac-GGTYSCHFGPLTWCKPKQG	2133	SPA2-PEG	7560	54
14	GGLYACMGPMTTWCKQPLRG	2177	SPA2-PEG	7862	30
18	SCHFGPLTWCK	1375	SPA2-PEG	7872	37
				6126	45

-28-

1.

EXAMPLE 2

5

PEG dimerization of peptide GGTYSCHFGPLTWVCKPQGG  
(SEQ ID NO: 8) (lot #1)

10

Examples 2 - 7 describe the dimerization of various peptides described by the present invention. The modification of peptide (SEQ ID NO: 8) was carried out by resuspending 25 mg (0.0071 mmol) of polymer in 4 ml PBS at pH 7.5, and adding a 3 fold molar excess of peptide (SEQ ID NO: 8) (0.0213 mmol, 44.5 mg, MW 2092) dissolved in 1 ml of 0.1% trifluoroacetic acid. The mixture was incubated on ice. After 3 hours of incubation, an additional 7.5 mg (0.0036 mmol) of lyophilized peptide was added, resulting in a final ratio of 3.5 moles of peptide per each mole of SPA2. The mixture was incubated an additional 17 hours on ice. The reaction mixture was adjusted to a final concentration of 50 mM Tris by the addition of 1 M tris-HCl of pH 7.5 and incubated on ice for 1 hour. The sample was subjected to analytical and preparative HPLC as described in Example 8. After preparative HPLC and lyophilization, 38 mg of PEG dimer was recovered. The theoretical yield for this experiment was 55 mg based on a calculated mass of 7600 mg/mmol for a yield of 69% (Table I).

20

25

30

35

-29-

1

EXAMPLE 3

5

PEG dimerization of peptide GGTYSCHFGPLTWVCKPQGG  
(SEQ ID NO: 8) (lot #2)

10

15

20

25

30

35

The modification of peptide (SEQ ID NO: 8) was carried out by resuspending 25 mg (0.0071 mmol) of polymer in 4 ml PBS at pH 7.5, and adding a ca. 3 fold molar excess of peptide (SEQ ID NO: 8) (0.0213 mmol, 45.8 mg, MW 2092) dissolved in 1 ml of 0.1% trifluoroacetic acid. The mixture was incubated on ice for 22 hours. At that time, the reaction was adjusted to a final concentration of 50 mM Tris by the addition of 1 M tris-HCl, pH 7.5. The reaction mixture was incubated on ice for 1 hour. The sample was subjected to analytical and preparative HPLC as described in Example 8. After preparative HPLC and lyophilization, 37 mg of PEG dimer was recovered. The theoretical yield for this experiment was 55 mg based on a calculated mass of 7600 mg/mmol for a yield of 68% (Table I).

-30-

1

EXAMPLE 4

5

PEG dimerization of peptide GGTYSCHFGPLTWVCKPQ  
(SEQ ID NO: 13)

10

The modification of peptide (SEQ ID NO: 13) was carried out by resuspending 11.2 mg (0.0033 mmol) of polymer in 2.5 ml PBS at pH 7.5, and adding a ca. 3 fold molar excess of peptide (SEQ ID NO: 13) (0.010 mmol, 20 mg, MW 1978) dissolved in 0.25 ml of 0.1% trifluoroacetic acid. The mixture was incubated on ice for 20 hours. At that time, 0.25 ml of 1 M tris-HCl at pH 7.5 was added. The reaction mixture was incubated at 4°C for one hour. The sample was subjected to analytical and preparative HPLC as described in Example 8. The main preparative reaction product peak eluted at ca 43 minutes. After preparative HPLC and lyophilization, 13.3 mg of PEG dimer was recovered. The theoretical yield for this experiment was 24.42 mg based on a calculated mass of 7400 mg/mmol for a yield of 54% (Table I).

15

20

25

30

35

-31-

1

EXAMPLE 5

5

PEG dimerization of peptide Ac-GGTY SCHFGPLTWVCKPQGG  
(SEQ ID NO: 20)

10

The modification of peptide (SEQ ID NO: 20) was carried out by resuspending 10.5 mg (0.0031 mmol) of polymer in 2.5 ml PBS at pH 7.5, and adding a ca. 3 fold molar excess of peptide (SEQ ID NO: 20) (0.0094 mmol, 20 mg, MW 2133) dissolved in 0.25 ml of 0.1% trifluoroacetic acid and the mixture incubated at 4°C for 28 hours. At that time, the reaction as monitored by HPLC was estimated to be approximately 30% complete, the temperature was shifted to ambient and an additional 27 hour incubation provided no net increase in product. Because of possible hydrolysis of the reactive polymer, an additional 5 mg of polymer was added and the incubation was continued for an additional 16 hours. At that time, 0.25 ml of 1 M tris-HCl, pH 7.5 was added and the reaction mix was incubated at 4°C for an additional 1 hour. The sample was subjected to analytical and preparative HPLC using a flatter gradient system as described in Example 8. The main preparative reaction product peak eluting at ca 48 minutes. After preparative HPLC and lyophilization, 10.4 mg of PEG dimer was recovered. The theoretical yield for this experiment was 34.4 mg based on a calculated mass of 7650 mg/mmol for a yield of 30% (Table I).

20

25

30

35

-32-

1

EXAMPLE 6

PEG dimerization of peptide (SEQ ID NO: 14)

5

The modification of peptide (SEQ ID NO: 14) was carried out by resuspending 2.6 mg (0.00076 mmol) of polymer in 3.0 ml PBS at pH 7.5 and adding a ca. 3 fold molar excess of peptide (SEQ ID NO: 14) (0.00229 mmol, 5 mg, MW 2177) dissolved in 0.1 ml of 0.1% trifluoroacetic acid. The mixture was incubated on ice for 26 hours.

10

At that time, 0.25 ml of 1 M-tris-HCl at pH 7.5 was added. The reaction mixture was incubated at 4°C for 1 hour. The sample was subjected to analytical and preparative HPLC using the flatter gradient system described in Example 8. The main preparative reaction product peak eluted at ca 46 minutes. After preparative HPLC and lyophilization, 2.2 mg of PEG dimer was recovered. The theoretical yield for this experiment was 24.42 mg based on a calculated mass of 7400 mg/mmol for a yield of 37% (Table I).

15

20

25

30

35

-33-

1

EXAMPLE 7

PEG dimerization of peptide (SEQ ID NO: 18)

5

The modification of peptide (SEQ ID NO: 18) was carried out by resuspending 1.2 mg (0.00036 mmol) of polymer in 0.5 ml PBS at pH 7.5, and adding a ca. 3 fold molar excess of the peptide (0.0011 mmol, 1.5 mg, MW 2177) dissolved in 0.05 ml of 0.1% trifluoroacetic acid. The mixture was incubated on ice for 20 hours. At that time, 0.1 ml of 1 M tris-HCl at pH 7.5 was added. The reaction mixture was incubated at 4°C for 1 hour. The sample was subjected to purification using an analytical HPLC system as described in Example 8. The main reaction product peak eluted at ca 38 minutes. After preparative HPLC and lyophilization, 1 mg of PEG dimer was recovered. The theoretical yield for this experiment was 2.2 mg based on a calculated mass of 6150 mg/mmol for a yield of 45% (Table I).

10

15

20

25

30

35

-34-

1

EXAMPLE 8

Analytical and Preparative HPLC analysis

5       The accumulation of the dimers described above  
in Examples 1-7 was monitored by analytical reverse  
phase HPLC. The analysis was carried out using a Vydac  
C-18 Protein-Peptide column (0.46 x 25 cm, part no.  
10      218TP54) and a Rainin Gradient HPLC system fitted with a  
Dynamax dual wavelength detector. At injection, the  
column was equilibrated in 0.1% TFA in dH<sub>2</sub>O and was  
developed with a 45 minute linear gradient (0-100%) of  
15      acetonitrile (ACN) containing 0.1% TFA beginning at 10  
minutes after injection. The flow rate was held  
constant at 1 ml/min. Under these analytical  
conditions, the SPA2 polymer and tris inactivated  
polymer did not appear to bind the column while a major  
reaction product with a retention time (37 minutes) was  
20      identified (Figure 1). Peptide (SEQ ID NO: 8)  
demonstrated a retention time of 35 minutes and the  
excess peptide utilized in the reaction was clearly  
distinguished from the nascent reaction products.

25      The main product reaction product peak was  
purified by preparative reverse phase HPLC on the same  
chromatographic system using a Vydac C-18 Protein-  
Peptide column (2.2 x 25 cm, part no. 218TP15022).  
Injection of the reaction mix (6 ml) occurred with the  
column equilibrated at 80:20, H<sub>2</sub>O:ACN (both containing  
30      0.1% TFA) at a constant flow rate of 8 ml/min. After a  
20 minute wash, the column was developed by application  
of a linear gradient of 100% ACN/0/1% TFA over 60

-35-

1 minutes. The major product peak eluting at 48 minutes  
was collected and lyophilized (Figure 2). These elution  
conditions were subsequently modified to improve the  
resolution of some conjugation products peptide (SEQ ID  
5 NO: 20), mPEG-peptide (SEQ ID NO: 8), peptide (SEQ ID  
NO: 14) from reaction by products. This was  
accomplished by application of a flatter linear gradient  
of 20-80% B over 60 minutes. The variation in retention  
time due to different peptides and elution condition is  
10 described as part of each synthesis example. The  
materials recovered from the main product peak from each  
reaction were subsequently analyzed by analytical  
reverse phase HPLC, MALDI-TOF mass spectrometry, EPO  
15 competitive binding potential and for in vitro  
bioactivity.

The activated PEG used in these experiments  
has an approximate molecular weight of 3400 and has  
amine reactive succinimidyl groups on either end of the  
difunctional linear polymer. This reactivity was  
20 employed to couple two equivalents of peptide (SEQ ID  
NO: 8) (MW= 2092) to the polymer with the concomitant  
liberation of two succinimidyl moieties resulting in a  
dimeric product as shown in Scheme I. Peptide (SEQ ID  
NO: 8) contains two potentially reactive amines, one at  
25 the N-terminus of the peptide and one in the side chain  
of the single lysine within the peptide sequence, so  
that a number of different connectivities between the  
two molecules was possible.

30 MALDI-TOF mass spectral analysis was  
supportive of the presence of the expected dimeric  
product (Figure 3) as indicated by a predominant species.

-36-

1 with a centroid mass of 7661. This data shows that the  
dimeric product described in the present invention was  
produced using the methods described herein.

5

10

15

20

25

30

35

-37-

1

EXAMPLE 9

5

This example demonstrates the interaction of peptide (SEQ ID NO: 8), peptide (SEQ ID NO: 16), peptide (SEQ ID NO: 18) and peptide (SEQ ID NO: 13) with EPO binding protein (EBP) using a bifunctional sulphhydryl reactive crosslinker, (1,4-Di-[3'-(2'-pyridyldithio)propionamido]butane DPDDB.

10

15

20

25

30

35

To explore the interaction of peptide (SEQ ID NO: 8) with EBP, a bifunctional sulphhydryl reactive crosslinker (DPDDB) was used in an attempt to stabilize a mimetic dependent dimeric structure. Control experiments demonstrated that the crosslinker does not inactivate the EPO binding potential of EBP or the proliferative properties of peptide (SEQ ID NO: 8). As shown in Figure 4, a dimeric EBP product was formed by co-incubation of the peptide, peptide (SEQ ID NO: 8), DPDDB and EBP. This data shows the ability of the peptide (SEQ ID NO: 8) to mediate formation of a soluble receptor dimer. To further explore this question, peptides (SEQ ID NO: 13), (SEQ ID NO: 16) and (SEQ ID NO: 18) were examined for their ability to mediate dimerization. As shown in Figure 4, lanes 7A and 8A, when peptide (SEQ ID NO: 13) was truncated at the carboxyl terminus, it retained good in vitro bioactivity and improved in vivo bioactivity, resulting in a crosslinking signal similar to peptide (SEQ ID NO: 8). However, peptide (SEQ ID NO: 18) did not appear to stabilize the dimerization signal (Figure 4, lanes 9A

- 38 -

1 and 10A) whereas peptide (SEQ ID NO: 16) (Figure 4,  
lanes 5A and 6A) gave a strong dimerization band. These  
two peptides differ by a single N-terminal tyrosine  
residue and display a similar profile in the in vitro  
5 proliferation assay with peptide (SEQ ID NO: 18) being  
inactive. Peptide (SEQ ID NO: 16) has an ED<sub>50</sub> of 3 μM  
on murine receptor cells. Both peptides have similar  
IC<sub>50</sub> values indicating that they both retain binding  
activity. These results demonstrate that EBP  
10 dimerization is a property of the EPO peptide series and  
that the presence of the tyrosine is critical for this  
activity and that this corresponds to in vitro  
bioactivity.

15

20

25

30

35

-39-

1

EXAMPLE 10

5

IMMOBILIZED EBP BASED [<sup>125</sup>I]EPO COMPETITION BINDING

ASSAY

10

This study examined the binding capacity of the EPO PEG dimers to bind EPO receptors.

15

The extracellular domain of the human erythropoietin receptor (EPO binding protein, EBP) was expressed and overproduced in E. coli. As with many other recombinant eukaryotic proteins produced in E. coli, the protein appeared as an insoluble product in laboratory scale fermentations and was refolded and purified to obtain active protein. EPO binding protein produced by this method contains one free sulfhydryl group which can be modified without effecting the solution phase binding of ligand. In order to immobilize the EPO binding protein for equilibrium binding analysis and for competition binding assay, the EPO binding protein was covalently attached to agarose beads.

20

25

The iodoacetyl activation chemistry of Sufolink beads (Pierce Chemical Co, Rockford, IL) is specific for free thiols and assures that the linkage is not easily reversible. EBP-Sufolink beads were made as follows: SulfoLink gel suspension (10 ml) was mixed with of coupling buffer (40 ml: 50 mM Tris, pH 8.3, 5 mM EDTA) and the gel was allowed to settle. The supernatant was removed and the EPO binding protein (0.3-1 mg/ml in coupling buffer) to be bound was added directly to the washed beads. The mixture was rocked

30

35

-40-

1 gently for 30 minutes at room temperature and the beads  
were allowed to settle for 1 hour at room temperature.  
The supernatant was removed and retained. The beads  
5 were washed twice with 20 ml of coupling buffer. The  
washes were recovered as well. The beads were then  
treated with 20 ml of 0.05 M cysteine for 30 minutes at  
room temperature to block unbound sites. Finally, the  
beads were washed with 50 ml of 1 M NaCl, then with 30  
10 ml of PBS, and resuspended in 20 ml of PBS and stored at  
4°C. The amount of EBP which was covalently bound to  
the beads was determined by comparing the OD<sub>280</sub> of the  
original EBP solution to the total OD<sub>280</sub> recovered in  
the reaction supernatant and the two 20 ml washes.  
Typically, 40-60% of the applied EBP remains associated  
15 with the beads.

Binding assays were initiated by the addition  
of EPO binding protein beads (50 µl) to individual  
reaction tubes. Total binding was measured in tubes  
containing 0.3-30 nM [<sup>125</sup>I]EPO (NEN Research Products,  
20 Boston MA, 100 µCi/µg). For determination of  
non-specific binding, unlabelled EPO was added at a  
level of 1000 fold in excess of the corresponding  
[<sup>125</sup>I]EPO concentration. Each reaction volume was  
brought to 500 µl with binding buffer (PBS/0.2% BSA).  
25 The tubes were incubated for five hours (a time period  
experimentally determined as adequate for the  
establishment of equilibrium) at room temperature with  
gentle rocking. After five hours, each reaction mixture  
was passed through a 1 ml pipet tip plugged with glass  
wool. The tubes were washed with 1 ml wash buffer (PBS/  
30 5% BSA) and this volume as well as 2 additional 1 ml

-41-

1      washes were passed through the pipet tip and collected  
for determination of the free EPO concentration.  
Equilibrium binding analysis of the specific association  
5      of [<sup>125</sup>I]EPO with EPO mimetic binding proteins  
immobilized on these agarose beads indicates a Kd of 5  
nM ± 2 based on a linear transformation (Scatchard) of  
the binding isotherm (Figure 5).

10     Competitive binding analysis assays of  
candidate peptides and dimer peptides were performed as  
outlined below. Individual peptides were dissolved in  
DMSO to prepare a stock solution 1 mM. Dimer peptides  
were contained within PBS at a concentration of 5 mM.  
All reaction tubes (in duplicate) contained 50 µL of EBP  
15     beads, 0.5 nM [<sup>125</sup>I]EPO and 0-500 µM peptide in a total  
of 500 µL binding buffer.

20     The final concentration of DMSO was adjusted  
to 2.5% in all peptide assay tubes. At this  
concentration DMSO has no detectable effect since an  
examination of the sensitivity of the assay to DMSO  
demonstrated that concentrations of up to 25% DMSO (v/v)  
had no deleterious effect on binding. Non-specific  
binding was measured in each individual assay by  
inclusion of tubes containing a large excess of  
25     unlabelled EPO (1000 nM). Initial assay points with no  
added peptide were included in each assay to determine  
total binding. Binding mixtures were incubated  
overnight at room temperature with gentle rocking. The  
beads were then collected using Micro-columns (Isolab,  
Inc.) and washed with 3 mL of wash buffer. The columns  
30     containing the washed beads were placed in 12 x 75 mm  
glass tubes and bound radioactivity levels determined in

-42-

1 a gamma counter. The amount of bound [<sup>125</sup>I]EPO was  
expressed as a percentage of the control (total=100%)  
binding and plotted versus the peptide concentration  
after correction for non-specific binding. The IC<sub>50</sub> was  
5 defined as the concentration of the analyte which  
reduced the binding of [<sup>125</sup>I]EPO to the EBP beads by  
50%. All data are reported as relative to peptide (SEQ  
ID NO: 8) which demonstrated an IC<sub>50</sub> of 5 μM.

10 Competitive binding analysis revealed an IC<sub>50</sub>  
of 20 μM for the purified dimer, a value four fold  
greater than peptide (SEQ ID NO: 8) in the same assay  
(Figure 5 and Table II). Polymer alone, which was  
inactivated by treatment with Tris-HCl, demonstrated a  
15 detectable competition binding signal but this signal  
was modest (<10%) at the IC<sub>50</sub> of the PEG-peptide (SEQ ID  
NO: 8) dimer.

20

25

30

35

-43-

TABLE II

Table II. Binding and Cell Proliferation Studies

id	Relative Binding*	EPO-ED <sub>50</sub> (μM)*	
		marine receptor	extracted human receptor
D. No. 8	1	0.1	0.09
ris inact. polymer	60	IA <sup>2</sup>	IA
sq. I.D. No. 8 covalent dimer #1	4	0.01 (10X)	0.0015 (60X)
sq. I.D. No. 8 covalent dimer #2	3	0.01 (10X)	0.002 (45X)
D. No. 13	1.6	0.08	0.02
sq. I.D. No. 13 covalent dimer	3	0.01 (8X)	0.002 (30X)
D. No. 20 (N-acetyl)	4	0.03	0.06
sq. I.D. No. 20 covalent dimer	12	0.2 (-7X)	0.05
D. No. 14 (terminal NH <sub>2</sub> )	0.6	0.1	0.08
sq. I.D. No. 14 covalent dimer	-	0.006 (16X)	0.001 (80X)

\* Amount required to achieve one half maximal level of EPO dependent proliferation (11 pM)

<sup>1</sup>Binding relative to Seq. I.D. No. 8

<sup>2</sup>Acanthocyte

Note that all peptides are cyclic and were analyzed as COOH terminal amides (-CONH<sub>2</sub>)

- 44 -

1

EXAMPLE 11

5

This example shows the improved potency of PEG-EPO peptide dimers to EPO receptors in human and murine cell lines.

10

Cell line FDC-P1/ER, an EPO-dependent line expressing the murine EPO receptor, was grown and maintained as described previously (Carroll et al.

15

1991). Also employed was cell line FDC-P1/trER expressing a functional truncated human EPO receptor (missing the C-terminal 40 amino acids). Both cell lines exhibit EPO dependent cellular proliferation.

20

Briefly, cells were maintained in RPMI 1640 media (Gibco/BRL) containing 10% heat-inactivated fetal calf serum and 10 units/ml of recombinant human EPO. For the cellular proliferation assay, FDC-P1/ER or FDC-P1/trER cells were grown to stationary phase, centrifuged,

washed with RPMI 1640 media (no EPO), and plated in EPO minus media for 24 hr.

25

After 24 hours, the cells were counted, resuspended at 800,000 cells/ml and dispensed at 40,000 cells/well. Stock solutions of the peptide dimer (5 mM in PBS) and peptide (10 mM in DMSO) were prepared and dispensed in triplicate to final concentrations of 1 x 10<sup>-10</sup> M through 1 x 10<sup>-5</sup> M and adjusted to a final volume of 0.2 ml. Final DMSO concentrations of 0.1% (V/V, maximal) or less were found to have no cellular toxicity or stimulatory effects. A standard EPO dose response curve was generated with each assay series.

-45-

1 After a 42 hr incubation at 37°C (ca. 2 cell doublings)  
1 $\mu$ Ci/well of [ $^3$ H] thymidine was added and the incubation  
continued for 6 hr at which time the cells were  
harvested and counted to assess [ $^3$ H]thymidine  
5 incorporation as a measure of cell proliferation.  
Results are expressed as the amount of peptide or dimer  
peptide necessary to yield one half of the maximal  
activity obtained with recombinant EPO.

10 As shown in Figure 5 and Table II, the initial  
lot of PEG-peptide (SEQ ID NO: 8) dimer demonstrated  
ED<sub>50</sub> values of 0.01  $\mu$ m and 0.0015  $\mu$ m in EPO responsive  
cell lines containing the murine or human EPO receptor,  
respectively. In both cell lines, the parent peptide,  
peptide (SEQ ID NO: 8), demonstrated an ED<sub>50</sub> of 0.1  $\mu$ M,  
15 indicating an increase in potency of 10 fold in the  
murine receptor line and almost 60 fold in the human  
receptor containing cells. Thus, the dimer was clearly  
more potent in murine and human lines than the peptides  
themselves. This was confirmed by generation of a  
20 second synthesis lot of PEG-peptide (SEQ ID NO: 8) dimer  
which resulted in a 10 and 45 fold increase in potency  
in the murine and human lines, respectively. Polymer  
alone, which was inactivated by treatment with Tris-HCl,  
demonstrated no activity in the cell proliferation  
25 assay.

A second EPO mimetic peptide, peptide (SEQ ID  
NO: 13), with the sequence GGTYSCHFGPLTWVCKPQ, was also  
subjected to a similar PEG dimerization protocol as that  
described above for peptide (SEQ ID NO: 8). The dimer  
30 product of PEG-peptide (SEQ ID NO: 13) is also more  
active than the unconjugated parent compound (Table II).

-46-

1 Both of these dimer peptides have ultimate ED<sub>50</sub> values  
near 0.002μM. In spite of this more modest increase,  
the experimental evidence clearly indicates that the  
dimerization of these peptides with PEG results in  
5 improved potency.

10

15

20

25

30

35

-47-

1

EXAMPLE 12

To further examine the connectivity of the peptides of the present invention to PEG, peptide molecules, which contained only an internal lysine group were used peptide (SEQ ID NO: 8) analog acetylated at the N-terminus peptide (SEQ ID NO: 20) and a sequence analog peptide (SEQ ID NO: 14) which only had a reactive N-terminal amine were PEG dimerized. In vitro proliferation data of these compounds suggest that potential dimerization through the free amino terminus has the most profound effect on bioactivity giving rise to a species about 80 fold more active than the monomeric parent peptide (SEQ ID NO: 14) dimer.

Conjugation through the lysine side chain had no real effect on activity peptide (SEQ ID NO: 20) as did mono-PEG or di-PEG conjugation (Table III). This data indicates that the creation of a head to head dimer (both peptides attached through the N-terminus) using a PEG linker greatly enhances the potency of EPO peptides and approaches a level almost two logs greater than the free parent peptide. Further, this effect was not observed upon simple covalent attachment of linear PEG to peptide (SEQ ID NO: 8) indicating that dimerization is a critical determinant for this increased activity.

30

35

- 4 8 -

TABLE III

Table III. Binding and Cell Proliferation Studies mPEG/

Compound	Relative Binding*	EPO-ED <sub>50</sub> (μM)*	
		stearic receptor	truncated human receptor
Seq. I.D. No. 8	1	0.1	0.09
mPEG/Seq. I.D. No. 8, peak #1	60	2	0.1
mPEG/Seq. I.D. No. 8, peak #2	>40	1	0.4

\* Amount required to achieve the half maximal level of EPO dependent proliferation (11 pM)

1 ND=Not determined

2 Adhesive

Binding relative = Seq. I.D. No. 8

Note that all peptides are cyclic and were analyzed as COOH terminal amides (-CONH<sub>2</sub>)

-49-

1

EXAMPLE 13

Polycythemic Exhypoxic Mouse Bioassay.

5        This study demonstrates the ability of peptide  
(SEQ ID NO: 8)/PEG-dimers to retain in vivo bioactivity.  
Peptides were assayed for in vivo activity in the  
polycythemic mouse bioassay adapted from the method  
described by Cotes and Bangham (1961), Nature 191: 1065-  
1067. BDF1 mice were allowed to acclimate to ambient  
10      conditions for 7-10 days. Body weights were determined  
for all animals. Low weight animals (<15 grams) were  
not used. Mice were introduced to hypobaric chambers  
with a 24 hour conditioning cycle consisting of 0.40%  
15      +/- 0.02 atm. for 18 hours followed by 6 hours at  
ambient pressure for a total of 14 days. Following the  
14 day period, mice were placed in ambient pressure for  
72 hours prior to dosing. Test samples or recombinant  
Human Erythropoietin (rHuEPO) standards were diluted in  
20      an assay vehicle consisting of Phosphate Buffered Saline  
(PBS)-0.1% Bovine Serum Albumin (BSA). Peptide sample  
stock solutions (excluding peptide dimers) were first  
solubilized in dimethyl sulfoxide (DMSO). Control  
groups included one group of vehicle alone, and one  
25      group of (DMSO) at final concentration of 1%.

Each dose group contained 10 mice. Mice were  
30      injected subcutaneously (scruff of neck) with 0.5 ml of  
the appropriate sample. Forty eight hours following the  
sample injection, the mice were administered an  
intraperitoneal injection of 0.2 ml of [<sup>59</sup>Fe]

35

-50-

1 (approximately 18.0 milliCuries/milligram, Dupont, NEN)  
and 0.75 microCuries/Mouse.

5 Mouse body weights were determined twenty four hours following [<sup>59</sup>Fe] administration and the mice were sacrificed forty eight hours following the [<sup>59</sup>Fe]  
injection. Blood was collected from each animal by  
10 cardiac puncture and hematocrits were determined (heparin was used as the anticoagulant). Each blood sample (0.2 ml) was analyzed for [<sup>59</sup>Fe] incorporation using a Packard gamma counter. Non-responder mice (i.e., those mice with radioactive incorporation less than the negative control group) were eliminated from the appropriate data set. Mice that had hematocrit values less than 53% were also eliminated.

15 This assay examined the ability of an exogenously administered compound to induce new red blood cell synthesis, or in other words to function as EPO or an EPO mimetic. The results are derived from sets of 10 animals for each experimental dose. As shown 20 in Figure 7 and Table IV, the data suggests that on a mole equivalent basis, peptide (SEQ ID NO: 8)/PEG-dimer is about 10 fold more active than peptide (SEQ ID NO: 8) monomer. These results are consistent with in vitro 25 results in which increased potency values of 10 fold was observed on murine EPO-R bearing cells.

TABLE IV

30 Table 4. Exhoxic Mouse Bioassay Study of PEG Dimer Activity

Compound	Amount required for equivalence to 0.025U EPO (nmol) n=10
Seq. I.D. No. 8	3.8

-51-

1

EXAMPLE 14

This example shows that an inactive truncation  
analog of peptide (SEQ ID NO: 8), which lacks the  
5 critical tyrosine peptide (SEQ ID NO: 18),  
(SCHFGPLTWVCK), can be converted to an agonist on the  
human EPO receptor cell line by PEG dimerization. In  
this experiment, a  $10^{-9}$  M concentration of the parent  
10 peptide had no activity above background while the  
dimeric peptide exhibited a level of proliferation twice  
as many cpm as background. As shown in Figure 8, the  
peptide alone (open squares) did not induce  
proliferation of the EPO responsive cells but upon PEG  
15 dimerization (open diamonds) a significant agonist  
effect was observed. Approximately twice as many cpm  
incorporated over non-stimulated cells at  $10^{-9}$  M added  
peptide dimer. The replicate error bars represent the  
standard deviation of three assay points per  
concentration of peptide or peptide dimer.

20

25

30

35

- 52 -

1      Exhypoxic polycythemic mouse bioassay:

PEG dimer and the monomer parent peptide RWJ 61718 were compared in the exhypoxic mouse bioassay (Table 1). This peptide exhibited an 80 fold increase in in vitro activity upon dimerization. Murine studies (in vivo) of the activity of the dimer compared to the monomer peptide revealed a 250 fold increase in activity of RWJ 61718 upon dimerization. Cellular proliferation studies on this dimer peptide in murine receptor containing cells demonstrated a 16 fold increase over the monomer indicating that the 250 fold increase in vivo might be attributable to other factors such as altered metabolism or prolonged circulatory half-life which occur upon PEG dimerization of the peptide sequence. Thus, in addition to the effect of dimerization alone, the PEG modification has an effect which impacts in vivo activity and may be specific to individual peptide sequences.

15

Cell associated EPO receptor competition binding assay.

A competitive binding analysis of the ability of selected monomer peptides and their cognate dimer products to compete with radiolabelled EPO binding for cell associated human EPO receptors was performed Erythropoietin Receptor Competition Binding Analysis was preformed as follows. TF-1 cells were maintained in RPMI 1640, 10% fetal calf serum, 1% L-glutamine, 1% penicillin, 0.1% streptomycin and 1 ng/ml of GM-CSF. [<sup>125</sup>I]-EPO was obtained from NEN Research Products. Cells were centrifuged and washed 1 x with binding buffer (RPMI 1640, 5% BSA, 25 mM Hepes, pH 7.5, 0.02% sodium azide) resuspended in binding buffer, and counted using trypan blue as an indicator of viability. Each reaction contained approximately 5 x 10<sup>5</sup> cells, [<sup>125</sup>I]-EPO (0.5 nM), no competitor or peptide or dimer preparation in a final volume of 200 µl. The binding reactions (in duplicate) were incubated overnight at 4°C. Following binding, the tubes were centrifuged at 12,000 rpm for 1 min at 4°C in a

35

-53-

1 refrigerated centrifuge. The supernatant was removed, the cell  
5 pellet resuspended in 100 µl of binding buffer, and the cell  
suspension layered onto 0.7 ml of bovine calf serum. The tubes were  
10 centrifuged at 12,000 rpm for 5 min at 4°C, the supernatant was  
removed, the bottom of the tubes snipped off, and the cell pellets  
15 counted in a Micromedic ME plus gamma counter. Non-specific binding  
was determined by incubating cells with [<sup>125</sup>I]-EPO and a 100-fold  
excess of non-radioactive EPO. These data demonstrate increases in  
apparent binding competitive affinity of 3.0 fold, 3.2 fold and 80  
fold for peptides RWJ 61233, RWJ 61596 and RWJ 61718, respectively  
(Table 2). In vivo proliferation studies with these peptides and  
their dimer derivatives reveal increases in potency of ea. 50 fold,  
10 fold and 80 fold, respectively, indicating that the magnitude of  
increased binding affinity is exceeded by the functional potency of  
the peptide for two of the three species. Thus, the effect of  
15 dimerization and subsequent increase in activity may be one in which  
the efficiency of receptor stimulation is improved by limiting the  
lateral diffusion of the receptors away from a binding event.  
Peptide dimerization therefore likely results in entropic rather  
than enthalpic gains upon mimetic ligand-receptor association for  
some peptide dimer sequences.

20  
25 Unlike the EBP-bead EPO competitive binding assay where peptide  
dimerization negatively impacted the ability of PEG dimer peptides  
to compete for receptor binding, the ability to compete for cell  
associated receptors is increased by dimerization. This may be due  
to the ability of the cell associated receptor to dimerize while the  
immobilized EBP monomer likely cannot.

30 Conversion of inactive to active peptide RWJ 61177 was further  
studied. An improved and expanded study was performed which  
confirmed our earlier observation of conversion to an active peptide  
(Figure 6, Panel D).

- 54 -

TABLE IV. EXHYPOXIC MOUSE BIOASSAY STUDY OF PEG DIMER ACTIVITY

Compound	Amount required for equivalency to 0.025 U EPO (nmol) n=10
RWJ 61233 (seq. ID #8)	3.8
SAP2/61233, covalent dimer	0.28
RWJ 61718 (seq. ID #14)	18
SAP2/61718, covalent dimer	0.07

- 55 -

TABLE V. EPO COMPETITIVE BINDING ANALYSIS OF CELL ASSOCIATED RECEPTORS

Compound	IC <sub>50</sub> (μM)
RWJ 61233 (seq ID #8)	3.8
SAP2/61233, covalent dimer	0.28
RWJ 61718 (seq ID#14)	18
SAP2/61718, covalent dimer	0.07

## SEQUENCE LISTING

## GENERAL INFORMATION:

i) APPLICANT: Johnson, Dana L  
Zivin, Robert A

ii) TITLE OF INVENTION: AGONIST PEPTIDE DIMERS

iii) NUMBER OF SEQUENCES: 93

iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Frank S. DiGiglio  
(B) STREET: 400 Garden City Plaza  
(C) CITY: Garden City  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 11530

v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/484,135  
(B) FILING DATE: 07-JUN-1995  
(C) CLASSIFICATION:

ii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: DiGiglio, Frank S  
(B) REGISTRATION NUMBER: 31,346  
(C) REFERENCE/DOCKET NUMBER: 9594

ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (516) 742-4343  
(B) TELEFAX: (516) 742-4366

## INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 57 -

c) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "Xaa(Pos1) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc; Xaa(Pos2) can be R,H,L or W; Xaa(Pos3) can be M,F or I; Xaa(Pos6) can be any one of the 20 L-amino acids or the stereoisomeric D-amino acids; Xaa(Pos9) can be D,E,I,L or V; and Xaa(Pos10) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc, provided that either Xaa(Pos1) or Xaa(Pos10) is C or Hoc"

i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa  
5 10

INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "Xaa(Pos2) and Xaa(Pos8) can be any one of the 20 L-amino acids; Xaa(Pos3) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc; Xaa(Pos4) can be R,H,L or W; Xaa(Pos5) can be M,F or I; Xaa(Pos11) can be D,E,I,L or V; and Xaa(Pos12) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc, provided that either Xaa(Pos3) or Xaa(Pos12) is C or Hoc"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Xaa Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa  
1 5 10

INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 58 -

;) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..16  
(D) OTHER INFORMATION: /note= "Xaa(Pos1), Xaa(Pos 3), Xaa(Pos9),  
Xaa(Pos14), Xaa(Pos15) and Xaa(Pos16) can be any one of 20  
L-amino acids; Xaa(Pos4) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid  
or Hoc; Xaa(Pos5) can be R,H,L or W; Xaa(Pos6) can be M,F or I;  
Xaa(Pos12) can be D,E,I,L or V; and Xaa(Pos13) can be C,A, $\alpha$ -  
amino- $\gamma$ -bromobutyric acid or Hoc, provided that either Xaa(Pos4)  
or Xaa(Pos13) is C or Hoc"

i) SEQUENCE DESCRIPTION: SEQ ID NO:3:

FORMATION FOR SEQ ID NO:4:

### i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Xaa Xaa  
 1 5 10 15

**INFORMATION FOR SEQ ID NO:5:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..16  
(D) OTHER INFORMATION: /note= "Xaa(Pos1), Xaa(Pos3) and Xaa(Pos16)  
can be any one of the 20 L-amino acids; Xaa(Pos5) can be R or H;  
Xaa(Pos6) can be F or M; Xaa(Pos9) can be I,L,T,M or V;  
Xaa(Pos12) can be D or V; Xaa(Pos14) can be C,W,I,L,R,S or T;  
Xaa(Pos15) can be A,G,P,R or Y"

- 59 -

i) SEQUENCE DESCRIPTION: SEQ ID NO:5:

aa Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Xaa Xaa  
5 10 15

FORMATION FOR SEQ ID NO:6:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

.i) MOLECULE TYPE: peptide

.x) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "Xaa(Pos1) can be D,E,L,N,S,T or V;  
Xaa(Pos3) can be A,H,K,L,M,S or T; Xaa(Pos5) can be R or H;  
Xaa(Pos6) can be F or M; Xaa(Pos9) can be I,L,T,M or V;  
Xaa(Pos12) can be D or V; Xaa(Pos14) can be K,R,S or T;  
Xaa(Pos15) is P and Xaa(Pos16) can be any one of the 20 L-amino  
acids"

xii) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Xaa Xaa  
1 5 10 15

NFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Leu Tyr Leu Cys Arg Phe Gly Pro Val Thr Trp Asp Cys Gly  
1 5 10 15

Tyr Lys Gly Gly  
20

- 60 -

FORMATION FOR SEQ ID NO:8:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

iii) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Iy Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
5 10 15

ro Gln Gly Gly  
20

FORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

iii) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Asp Tyr His Cys Arg Met Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15

Pro Leu Gly Gly  
20

FORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 61 -

## (i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Gly Asn Tyr Met Cys His Phe Gly Pro Ile Thr Trp Val Cys Arg  
1 5 10 15

Pro Gly Gly Gly  
20

## INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Gly Val Tyr Ala Cys Arg Met Gly Pro Ile Thr Trp Val Cys Ser  
1 5 10 15

Pro Leu Gly Gly  
20

## INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Gly Asn Tyr Met Ala His Met Gly Pro Ile Thr Trp Val Cys Arg  
1 5 10 15

Pro Gly Gly

## INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid

- 62 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- i) MOLECULE TYPE: peptide

- ii) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
5 10 15

ro Gln

FORMATION FOR SEQ ID NO:14:

- i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- ii) MOLECULE TYPE: peptide

- xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Gly Leu Tyr Ala Cys His Met Gly Pro Met Thr Trp Val Cys Gln  
1 5 10 15

Pro Leu Arg Gly  
20

INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Ile Ala Gln Tyr Ile Cys Tyr Met Gly Pro Glu Thr Trp Glu Cys  
1 5 10 15

Arg Pro Ser Pro Lys Ala  
20

## FORMATION FOR SEQ ID NO:16:

i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

hr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
5 10

## FORMATION FOR SEQ ID NO:17:

i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Cys His Phe Gly Pro Leu Thr Trp Val Cys  
1 5 10

## INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10

## INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids

-64-

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

c) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "Xaa(Pos1) can be any one of the 20 L-amino acids; except that Xaa(Pos1) may or may not be Y and Xaa(Pos1) may be any non-naturally occurring aromatic acid analog when Xaa(Pos1) is Y. Xaa(Pos2) and Xaa(Pos8) can be any one of the 20 L-amino acids; Xaa(Pos3) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc; Xaa(Pos4) can be R,H,L or W; Xaa(Pos5) can be M,F or I; Xaa(Pos11) can be D,E,I,L or V and Xaa(Pos12) can be C,A, $\alpha$ -amino- $\gamma$ -bromobutyric acid or Hoc provided that either Xaa(Pos3) or Xaa(Pos12) is C or Hoc"

ii) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa  
5 10

INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15  
Pro Gln Gly Gly  
20

INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

i) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ly Gly Thr Tyr Arg Cys Ser Met Gly Pro Met Thr Trp Val Cys Leu  
5 10 15

ro Met Gly Gly  
20

FORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Gly Met Tyr Ser Cys Arg Met Gly Pro Met Thr Trp Val Cys Gly  
1 5 10 15

Pro Ser Gly Gly  
20

FORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Gly Trp Ala Trp Cys Arg Met Gly Pro Ile Thr Trp Val Cys Ser  
1 5 10 15

Ala His Gly Gly  
20

## FORMATION FOR SEQ ID NO:24:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

.i) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Gly Met Tyr Ser Cys Arg Met Gly Pro Met Thr Trp Val Cys Ile  
1 5 10 15

Pro Tyr Gly Gly  
20

## INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Gly Glu Tyr Lys Cys Tyr Met Gly Pro Ile Thr Trp Val Cys Lys  
1 5 10 15

Pro Glu Gly Gly  
20

## INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 67 -

i) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ly Gly Asp Tyr Thr Cys Arg Met Gly Pro Met Thr Trp Ile Cys Thr  
5 10 15

.la Thr Gly Gly  
20

INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gly Gly Asn Tyr Leu Cys Arg Phe Gly Pro Gly Thr Trp Asp Cys Thr  
1 5 10 15

Gly Phe Arg Gly  
20

INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly Gly Asn Tyr Val Cys Arg Met Gly Pro Ile Thr Trp Ile Cys Thr  
1 5 10 15

Pro Ala Gly Gly  
20

INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- 68 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

ii) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Gly Lys Asp Val Cys Arg Met Gly Pro Ile Thr Trp Asp Cys Arg  
5 10 15  
Ser Thr Gly Gly  
20

INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gly Ser Tyr Leu Cys Arg Met Gly Pro Thr Thr Trp Leu Cys Thr  
1 5 10 15  
Ala Gln Arg Gly Gly Gly Asn  
20

INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Asn Tyr Leu Cys Arg Met Gly Pro Ala Thr Trp Val Cys Gly  
1 5 10 15  
Arg Met Gly Gly  
20

- 69 -

## FORMATION FOR SEQ ID NO:32:

i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

.i) MOLECULE TYPE: peptide

:ii) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Glu Tyr Lys Cys Arg Met Gly Pro Leu Thr Trp Val Cys Gln  
1 5 10 15  
Tyr Ala Gly Gly  
20

## NFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Gly Gly Asp Tyr Thr Cys Arg Met Gly Pro Met Thr Trp Ile Cys Thr  
1 5 10 15  
Ala Thr Arg Gly  
20

## INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

-70-

## (i) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Val Tyr Val Cys Arg Met Gly Pro Leu Thr Trp Glu Cys Thr  
1 5 10 15

Ala Ser Gly Gly  
20

## INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gly Glu Tyr Ser Cys Arg Met Gly Pro Met Thr Trp Val Cys Ser  
1 5 10 15

Pro Thr Gly Gly  
20

## INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Glu Tyr Leu Cys Arg Met Gly Pro Ile Thr Trp Val Cys Glu  
1 5 10 15

Arg Tyr Gly Gly  
20

## INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid

- 71 -

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

ii) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ly Gly Asn Tyr Ile Cys Arg Met Gly Pro Met Thr Trp Val Cys Thr  
5 10 15  
la His Gly Gly  
20

INFORMATION FOR SEQ ID NO:38:

i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Asp Tyr Leu Cys Arg Met Gly Pro Ala Thr Trp Val Cys Gly  
1 5 10 15  
Arg Met Gly Gly  
20

INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Gly Leu Tyr Leu Cys Arg Phe Gly Pro Val Thr Trp Asp Cys Gly  
1 5 10 15  
Tyr Lys Gly Gly  
20

-79-

## FORMATION FOR SEQ ID NO:40:

i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

i) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ly Gly Leu Tyr Ser Cys Arg Met Gly Pro Ile Thr Trp Val Cys Thr  
5 10 15

ys Ala Gly Gly  
20

## FORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gly Gly Gly Tyr His Cys Arg Met Gly Pro Met Thr Trp Val Cys Arg  
1 5 10 15

Pro Val Gly Gly  
20

## FORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

-73-

) SEQUENCE DESCRIPTION: SEQ ID NO:42:

y Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
5 10 15

:o Gln Gly Gly  
20

FORMATION FOR SEQ ID NO:43:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

iii) SEQUENCE DESCRIPTION: SEQ ID NO:43:

:ly Gly Ile Tyr Lys Cys Leu Met Gly Pro Leu Thr Trp Val Cys Thr  
5 10 15

:ro Asp Gly Gly  
20

FORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Gly Gly Leu Tyr Ser Cys Leu Met Gly Pro Ile Thr Trp Leu Cys Lys  
1 5 10 15

Pro Lys Gly Gly  
20

FORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Asp Tyr His Cys Arg Met Gly Pro Leu Thr Trp Val Cys Lys  
5 10 15

Leu Gly Gly  
20

FORMATION FOR SEQ ID NO:46:

- i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

i) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Asp Tyr Ser Cys Arg Met Gly Pro Thr Thr Trp Val Cys Thr  
5 10 15

Pro Pro Gly Gly  
20

FORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly Gly Asp Tyr Trp Cys Arg Met Gly Pro Ser Thr Trp Glu Cys Asn  
1 5 10 15

Ala His Gly Gly  
20

-78-

## FORMATION FOR SEQ ID NO:48:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

.i) MOLECULE TYPE: peptide

:i) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gly Gly Lys Tyr Leu Cys Ser Phe Gly Pro Ile Thr Trp Val Cys Ala  
1 5 10 15

Arg Tyr Gly Gly  
20

## INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gly Gly Leu Tyr Lys Cys Arg Leu Gly Pro Ile Thr Trp Val Cys Ser  
1 5 10 15

Pro Leu Gly Gly  
20

## INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 76 -

i) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gly Ser Tyr Thr Cys Arg Phe Gly Pro Glu Thr Trp Val Cys Arg  
5 10 15

Pro Asn Gly Gly  
20

INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Gly Ser Tyr Ser Cys Arg Met Gly Pro Ile Thr Trp Val Cys Lys  
1 5 10 15

Pro Gly Gly Gly  
20

INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Gly Ser Tyr Thr Cys Arg Met Gly Pro Ile Thr Trp Val Cys Leu  
1 5 10 15

Pro Ala Gly Gly  
20

INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

-77-

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

ii) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Gly Leu Tyr Glu Cys Arg Met Gly Pro Met Thr Trp Val Cys Arg  
1                   5                   10                   15  
Pro Gly Gly Gly  
20

INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Asp Tyr Thr Cys Arg Met Gly Pro Ile Thr Trp Ile Cys Thr  
1                   5                   10                   15  
Lys Ala Gly Gly  
20

INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Gly Val Tyr Ser Cys Arg Met Gly Pro Thr Thr Trp Glu Cys Asn  
1                   5                   10                   15  
Asn Tyr Val Gly  
20

-78-

## INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Gly Ala Tyr Leu Cys His Met Gly Pro Ile Thr Trp Val Cys Arg  
1                   5                   10                   15

Pro Gln Gly Gly  
20

## INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Gly Gly Glu Tyr Ser Cys Arg Met Gly Pro Asn Thr Trp Val Cys Lys  
1                   5                   10                   15

Pro Val Gly Gly  
20

## INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

-79-

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

ii) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ly Gly Val Tyr Lys Cys Arg Met Gly Pro Leu Thr Trp Glu Cys Arg  
5 10 15  
ro Thr Gly Gly  
20

INFORMATION FOR SEQ ID NO:62:

- i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xii) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Gly Gly Asp Tyr Asn Cys Arg Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15  
Pro Ser Gly Gly  
20

INFORMATION FOR SEQ ID NO:63:

- i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xiii) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Gly Ser Tyr Leu Cys Arg Phe Gly Pro Thr Thr Trp Leu Cys Ser  
1 5 10 15  
Ser Ala Gly Gly  
20

- 80 -

i) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gly Leu Tyr Leu Cys Arg Met Gly Pro Val Thr Trp Glu Cys Gln  
5 10 15  
Pro Arg Gly Gly  
20

FORMATION FOR SEQ ID NO:59:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

.i) MOLECULE TYPE: peptide

:i) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gly Gly Leu Tyr Thr Cys Pro Met Gly Pro Ile Thr Trp Val Cys Leu  
1 5 10 15  
Leu Pro Gly Gly  
20

NFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

:xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Gly Leu Tyr Thr Cys Arg Met Gly Pro Val Thr Trp Val Cys Thr  
1 5 10 15  
Gly Ala Gly Gly  
20

INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- 31 -

## i) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ly Gly Trp Val Thr Cys Arg Met Gly Pro Ile Thr Trp Val Cys Gly  
5 10 15

al His Gly Gly  
20

## INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Gly Gly Gln Leu Leu Cys Gly Ile Gly Pro Ile Thr Trp Val Cys Arg  
1 5 10 15

Trp Val Gly Gly  
20

## INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gly Gly Lys Tyr Ser Cys Phe Met Gly Pro Thr Thr Trp Val Cys Ser  
1 5 10 15

Pro Val Gly Arg Gly Val  
20

## INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- 82 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:77:

Gly Leu Tyr Leu Cys Arg Met Gly Pro Gln Thr Trp Met Cys Gln  
5 10 15

o Gly Gly Gly  
20

FORMATION FOR SEQ ID NO:78:

- i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

i) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ly Gly Asp Tyr Val Cys Arg Met Gly Pro Met Thr Trp Val Cys Ala  
5 10 15

ro Tyr Gly Arg  
20

FORMATION FOR SEQ ID NO:79:

- ii) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Gly Trp Tyr Ser Cys Leu Met Gly Pro Met Thr Trp Val Cys Lys  
1 5 10 15

Ala His Arg Gly  
20

-83-

## FORMATION FOR SEQ ID NO:80:

i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

iii) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gly Gly Lys Tyr Tyr Cys Trp Met Gly Pro Met Thr Trp Val Cys Ser  
1                   5                   10                   15

Pro Ala Gly Gly  
20

## INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Gly Tyr Val Met Cys Arg Ile Gly Pro Ile Thr Trp Val Cys Asp  
1                   5                   10                   15

Ile Pro Gly Gly  
20

## INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 84 -

## (i) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Ser Cys Leu Gln Cys Cys Ile Gly Pro Ile Thr Trp Val Cys Arg  
5 10 15

Ile Ala Gly Gly  
20

## INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Gly Gly Asn Tyr Phe Cys Arg Met Gly Pro Ile Thr Trp Val Cys Gln  
1 5 10 15

Arg Ser Val Gly  
20

## INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Gly Gly Glu Tyr Ile Cys Arg Met Gly Pro Leu Thr Trp Glu Cys Lys  
1 5 10 15

Arg Thr Gly Gly  
20

## INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- 85 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Gly Gly Leu Tyr Ala Cys Arg Met Gly Pro Ile Thr Trp Val Cys Lys  
1                   5                   10                   15  
Tyr Met Ala Gly  
                    20

INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Gly Gln Tyr Leu Cys Thr Phe Gly Pro Ile Thr Trp Leu Cys Arg  
1                   5                   10                   15  
Gly Ala Gly Gly  
                    20

INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gly Gly Val Tyr Ala Cys Arg Met Gly Pro Ile Thr Trp Val Cys Ser  
1                   5                   10                   15  
Pro Leu Gly Gly  
                    20

- 86 -

INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Gly Gly Tyr Thr Thr Cys Arg Met Gly Pro Ile Thr Trp Val Cys Ser  
1 5 10 15

Ala His Gly Gly  
20

INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gly Gly Thr Tyr Lys Cys Trp Met Gly Pro Met Thr Trp Val Cys Arg  
1 5 10 15

Pro Val Gly Gly  
20

INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 87 -

## i) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gly Asn Tyr Tyr Cys Arg Phe Gly Pro Ile Thr Phe Glu Cys His  
5 10 15

to Thr Gly Gly  
20

## FORMATION FOR SEQ ID NO:91:

## i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## .i) MOLECULE TYPE: peptide

## .ii) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Gly Gly Glu Tyr Leu Cys Arg Met Gly Pro Asn Thr Trp Val Cys Thr  
1 5 10 15

Pro Val Gly Gly  
20

## INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## ii) MOLECULE TYPE: peptide

## .xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Gly Gly Leu Tyr Thr Cys Arg Met Gly Pro Ile Thr Trp Val Cys Leu  
1 5 10 15

Pro Ala Gly Gly  
20

## INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- 88 -

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Gly Leu Tyr Thr Cys Arg Met Gly Pro Ile Thr Trp Val Cys Leu  
1 5 10 15

Pro Ala Gly Gly  
20

- 89 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gly Gly Trp Val Tyr Cys Arg Ile Gly Pro Ile Thr Trp Val Cys Asp  
1                   5                   10                   15  
Thr Asn Gly Gly  
20

INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Gly Gly Met Tyr Tyr Cys Arg Met Gly Pro Met Thr Trp Val Cys Lys  
1                   5                   10                   15  
Gly Ala Gly Gly  
20

INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Gly Thr Thr Gln Cys Trp Ile Gly Pro Ile Thr Trp Val Cys Arg  
1                   5                   10                   15  
Ala Arg Gly Gly  
20

-90-

FORMATION FOR SEQ ID NO:72:

i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

iii) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Gly Pro Tyr His Cys Arg Met Gly Pro Ile Thr Trp Val Cys Gly  
5 10 15

Pro Val Gly Gly  
20

FORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Gly Glu Tyr Arg Cys Arg Met Gly Pro Ile Ser Trp Val Cys Ser  
1 5 10 15

Pro Gln Gly Gly  
20

FORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 91 -

## I) SEQUENCE DESCRIPTION: SEQ ID NO:74:

y Gly Asn Tyr Thr Cys Arg Phe Gly Pro Leu Thr Trp Glu Cys Thr  
5 10 15

o Gln Gly Gly Gly Ala  
20

## FORMATION FOR SEQ ID NO:75:

## i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

i) MOLECULE TYPE: peptide

## ii) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ly Gly Ser Trp Asp Cys Arg Ile Gly Pro Ile Thr Trp Val Cys Lys  
5 10 15

rp Ser Gly Gly  
20

## FORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

## xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Val Gly Asn Tyr Met Cys His Phe Gly Pro Ile Thr Trp Val Cys Arg  
1 5 10 15

Pro Gly Gly Gly  
20

## FORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

-92-

1

WE CLAIM:

5           1. A peptide dimer comprising two monomeric peptides of 10 to about 40 amino acids in length that bind to EPO receptor, each monomeric peptide comprising a sequence of amino acids X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub> (SEQ ID NO: 1) wherein X<sub>6</sub> is selected from any of the 20 genetically coded L-amino acids; X<sub>3</sub> is C; X<sub>4</sub> is R, H, L or W; X<sub>5</sub> is M, F or I; X<sub>7</sub> is D, E, I, L or V; and X<sub>8</sub> is C.

10

15           2. The peptide dimer of Claim 1 wherein each of said monomeric peptides comprise a sequence of amino acids YX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub>, (SEQ ID NO: 2) wherein each of X<sub>2</sub> and X<sub>6</sub> is independently selected from any one of the 20 genetically coded L-amino acids; X<sub>3</sub> is C; X<sub>4</sub> is R, H, L or W; X<sub>5</sub> is M, F or I; X<sub>7</sub> is D, E, I, L or V; and X<sub>8</sub> is C.

15

20           3. The peptide dimer of Claim 2 wherein each of said monomeric peptides comprise a sequence of amino acids X<sub>1</sub>YX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub>X<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 3) wherein each of X<sub>1</sub>, X<sub>2</sub>, X<sub>6</sub>, X<sub>9</sub>, X<sub>10</sub>, and X<sub>11</sub> is independently selected from any one of the 20 genetically coded L-amino acids; X<sub>3</sub> is C; X<sub>4</sub> is R, H, L or W; X<sub>5</sub> is M, F or I; X<sub>7</sub> is D, E, I, L or V; and X<sub>8</sub> is C.

25

25           4. The peptide dimer of Claim 3 wherein X<sub>4</sub> is R or H; X<sub>5</sub> is F or M; X<sub>6</sub> is I, L, T, M or V; X<sub>7</sub> is D or V; X<sub>9</sub> is G, K, L, Q, R, S, or T; and X<sub>10</sub> is A, G, P, R, or Y.

30

30           5. The peptide dimer of Claim 4 wherein X<sub>1</sub> is D, E, L, N, S, T or V; X<sub>2</sub> is A, H, K, L, M, S, or T; X<sub>8</sub> is R or H; X<sub>9</sub> is K, R, S, or T; and X<sub>10</sub> is P.

35

-93-

6. The peptide dimer of Claim 1 wherein said monomeric peptides are

GGLYLCRFGPVTWDCGYKGG (SEQ ID NO: 7);  
GGTYSCHFGPLTWVCKPQGG (SEQ ID NO: 8);  
GGDYHCRMGPPLTWVCKPLGG (SEQ ID NO: 9);  
VGNYMCHFGPITWVCRPGGG (SEQ ID NO: 10);  
GGVYACRMGPITWVCSPPLGG (SEQ ID NO: 11);  
VGNYMAHMGPITWVCRPGG (SEQ ID NO: 12);  
GGTYSCHFGPLTWVCKPQ (SEQ ID NO: 13);  
GGLYACHMGPMTWVCQPLRG (SEQ ID NO: 14);  
TIAQYICYMGPETWECRPSPKA (SEQ ID NO: 15);  
YSCHFGPLTWVCK (SEQ ID NO: 16);  
YCHFGPLTWVC (SEQ ID NO: 17); and  
SCHFGPLTWVCK (SEQ ID NO: 18)

7. A pharmaceutical composition comprising at least one peptide dimer of any one of Claims 1-6.

8. A method for treating a patient having a disorder characterized by a deficiency of EPO or low or defective red blood cell population comprising administering to said patient a therapeutically effective amount of at least one peptide dimer of any one of Claims 1-6.

9. The peptide dimer of any one of Claims 1-6 wherein said dimer is formed by a polyethylene glycol linker through a covalent bond.

10. The peptide dimer of any one of Claims 1-6 wherein said monomeric peptide units are dimerized on activated benodiazepins, oxazalones, azalactones, aminimides or diketopiperazine.

-94-

1

11. The peptide dimer of Claim 9 wherein said monomeric peptides are covalently bound N-terminus to N-terminus.

5

12. The peptide dimer of Claim 10 wherein said monomeric peptides are covalently bound N-terminus to N-terminus.

10

13. The peptide dimer of Claim 9 wherein said monomeric peptides are covalently bound N-terminus to C-terminus.

15

14. The peptide of Claim 10 wherein said monomeric peptides are covalently bound N-terminus to C-terminus.

20

15. A method of improving the bioactivity of a cell surface receptor comprising dimerizing a monomeric agonist of said cell surface receptor and contacting said formed dimer with said cell surface receptor to effect said improved biological activity.

25

16. A method of activating a cell surface receptor to induce biological activity of said cell surface receptor comprising dimerizing a monomeric agonist of said cell surface receptor and contacting said formed dimer with said receptor thereby inducing said biological activity.

30

17. The method of Claim 15 or 16 wherein said cell surface receptor is contacted with said dimer in vitro or in vivo.

18. The method of Claim 15 or 16 wherein said cell surface receptor is EPO-R.

35

19. The method of Claim 15 or 16 wherein said cell surface agonist is a GH agonist, PDGF agonist, IGF agonist, G-CSF agonist, TPO agonist, VEGF agonist, FGF

-95-

1

agonist, insulin agonist, IL-3 agonist, IL-5 agonist, IL-6 agonist or IL-2 agonist.

5

20. The method of Claim 15 or 16 wherein said agonist comprises a sequence of amino acids YX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub>, (SEQ ID NO: 2) wherein each of X<sub>2</sub> and X<sub>6</sub> is independently selected from any one of the 20 genetically coded L-amino acids; X<sub>3</sub> is C; X<sub>4</sub> is R, H, L or W; X<sub>5</sub> is M, F or I; X<sub>7</sub> is D, E, I, L or V; and X<sub>8</sub> is C.

10

21. The method of Claim 15 or 16 wherein said agonist comprises a sequence of amino acids X<sub>1</sub>YX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub>X<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 3) wherein each of X<sub>1</sub>, X<sub>2</sub>, X<sub>6</sub>, X<sub>9</sub>, X<sub>10</sub>, and X<sub>11</sub> is independently selected from any one of the 20 genetically coded L-amino acids; X<sub>3</sub> is C; X<sub>4</sub> is R, H, L or W; X<sub>5</sub> is M, F or I; X<sub>7</sub> is D, E, I, L or V; and X<sub>8</sub> is C.

15

22. The method of Claim 15 or 16 wherein said agonist comprises a sequence of amino acids X<sub>1</sub>Y<sub>1</sub>X<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub>X<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 3) wherein each of X<sub>1</sub>, X<sub>2</sub> and X<sub>11</sub> is independently selected from any one of the 20 genetically coded L-amino acids; X<sub>3</sub> is C; X<sub>4</sub> is R or H; X<sub>5</sub> is F or M; X<sub>6</sub> is I, L, T, M or V; X<sub>7</sub> is D or V; X<sub>8</sub> is G, K, L, Q, R, S, or T; and X<sub>10</sub> is A, G, P, R, or Y.

25

30

23. The method of Claims 15 or 16 wherein said agonist comprises a sequence of amino acids X<sub>1</sub>YX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>X<sub>5</sub>GPX<sub>6</sub>TWX<sub>7</sub>X<sub>8</sub>X<sub>9</sub>X<sub>10</sub>X<sub>11</sub> (SEQ ID NO: 3) wherein X<sub>1</sub> is D, E, L, N, S, T or V; X<sub>2</sub> is A, H, K, L, M, S, or T; X<sub>3</sub> is C; X<sub>4</sub> is R or H; X<sub>5</sub> is M, F or I; X<sub>6</sub> and X<sub>11</sub> are independently any one of the 20 genetically coded L-

-96-

1 amino acids; X<sub>7</sub> is D, E, I, L or V; X<sub>8</sub> is C; X<sub>9</sub> is K, R, S, or T; and X<sub>10</sub> is P.

24. The method of Claim 15 or 16 wherein said agonist is selected from the group consisting of:

5 GGLYLCRFGPVTWDCGYKGG (SEQ ID NO: 7);  
GGTYSCHFGPLTWVCKPQGG (SEQ ID NO: 8);  
GGDYHCRMGPLTWVCKPLGG (SEQ ID NO: 9);  
VGNYMCHFGPITWVCRPCGGG (SEQ ID NO: 10);  
10 GGVYACRMGPITWVCSPPLGG (SEQ ID NO: 11);  
VGNYMAHMGPITWVCRPCGG (SEQ ID NO: 12);  
GGTYSCHFGPLTWVCKPQ (SEQ ID NO: 13);  
GGLYACHMGPMTWVCQPLRG (SEQ ID NO: 14);  
TIAQYICYMGPETWECRSPKA (SEQ ID NO: 15);  
15 YSCHFGPLTWVCK (SEQ ID NO: 16); and  
YCHFGPLTWVC (SEQ ID NO: 17).

20 25. The method of Claim 15 or 16 wherein said peptide dimers are formed with a polyethylene glycol linker through a covalent bond.

26. A method of preparing a cell surface receptor agonist comprising dimerizing a cell surface antagonist.

25 30 35. The method of Claim 26 wherein said cell surface antagonist receptor is a GH antagonist, PDGF antagonist, EGF antagonist, G-CSF antagonist, EGF antagonist, GM-CSF antagonist, TPO antagonist, VEGF antagonist, FGF antagonist, insulin antagonist, IL-3 antagonist, IL-5 antagonist, IL-6 antagonist, or an IL-2 antagonist.

30 35. The method of Claim 26 wherein said cell surface receptor antagonist is a EPO-R antagonist.

-97-

1

29. The method of Claim 28 wherein said antagonist comprises a sequence of amino acids  $(AX_2)_nX_3X_4X_5GPX_6TWX_7X_8$  (SEQ ID NO: 19) wherein  $X_6$  is selected from any of the 20 genetically coded L-amino acids;  $X_3$  is C;  $X_4$  is R, H, L or W;  $X_5$  is M, F or I;  $X_7$  is D, E, I, L or V;  $X_8$  is C;  $X_2$  is selected from any of the 20 genetically coded L-amino acids, n is 0 or 1 and A is any of the 20 genetically coded L-amino acids except Y (tyrosine).

10

30. The method of Claim 21 where said antagonist is SCHFGPLTWVCK (SEQ ID NO: 18).

15

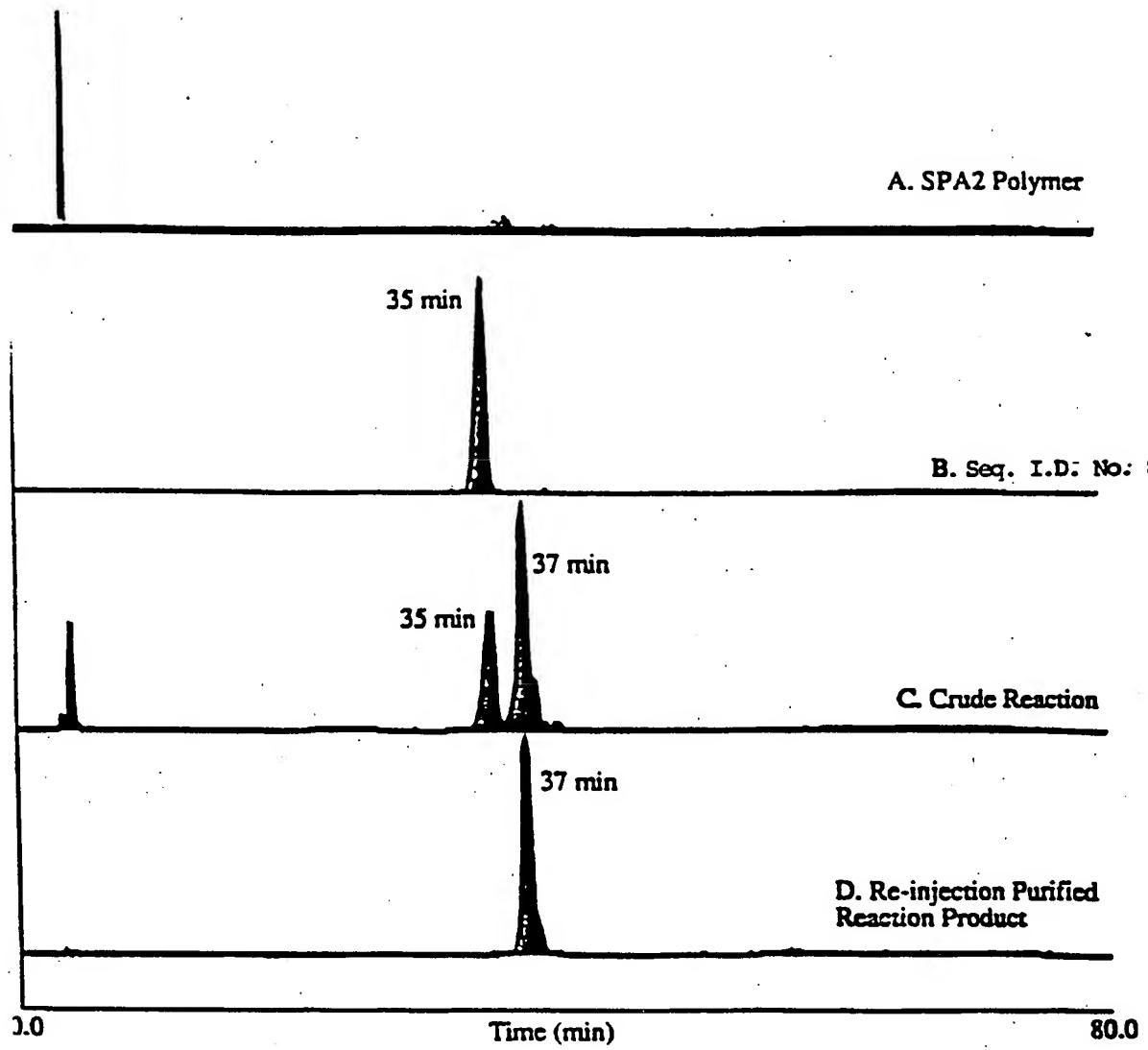
20

25

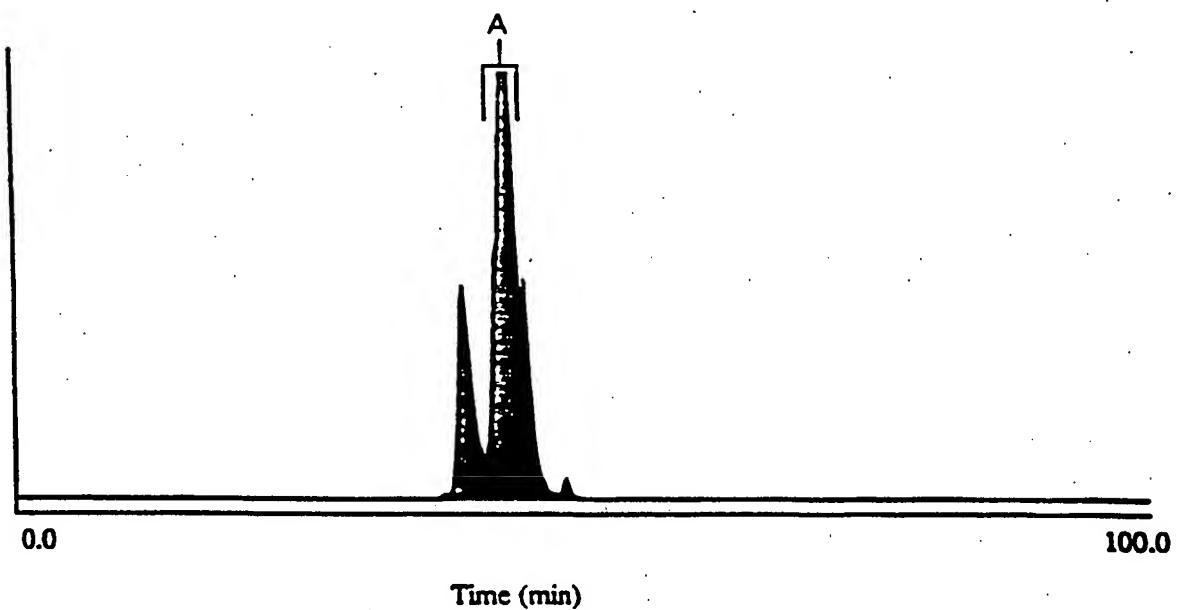
30

35

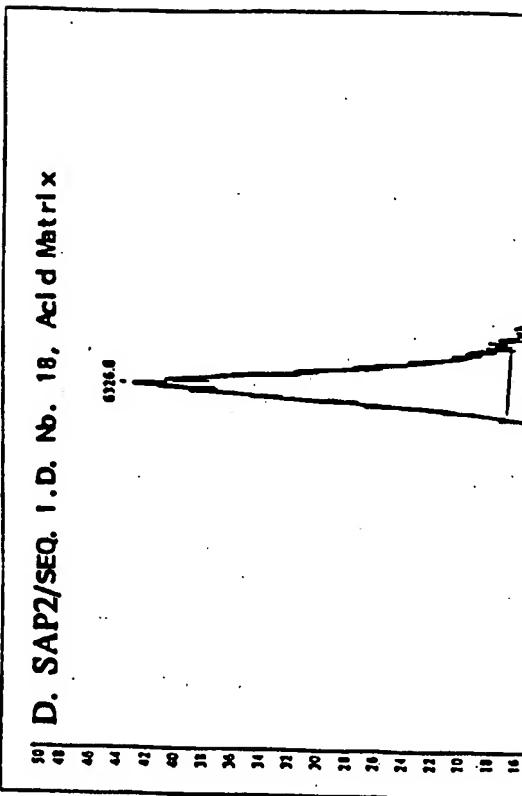
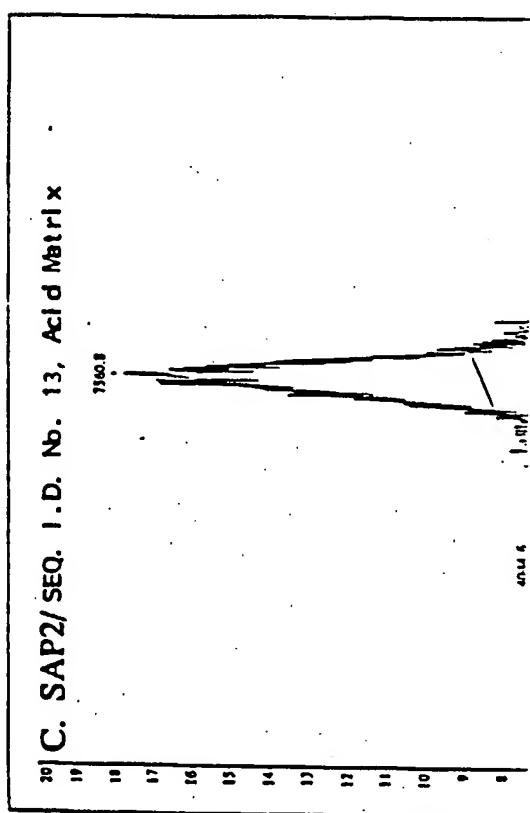
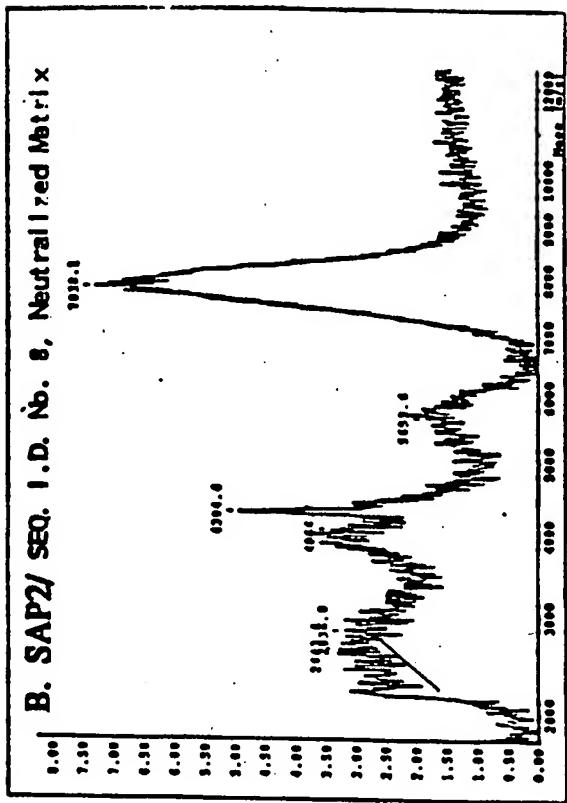
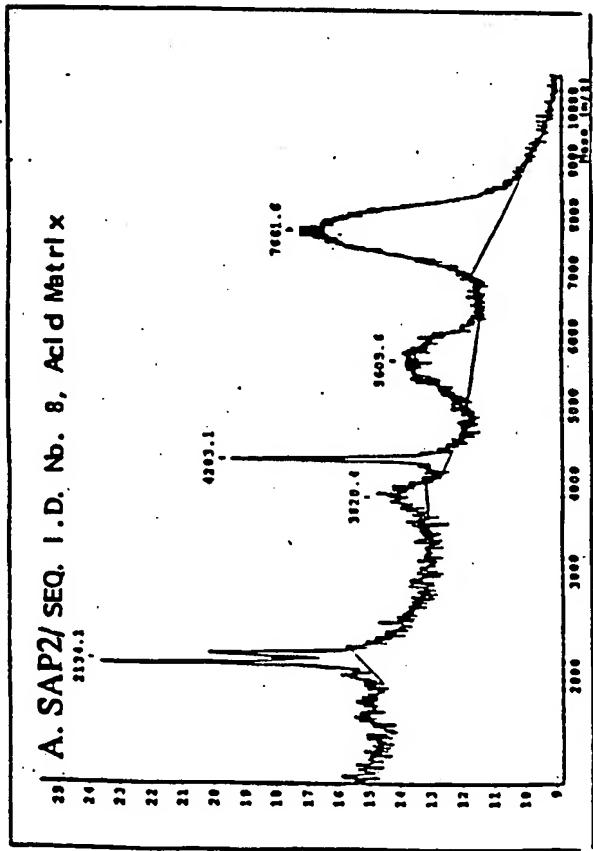
1/12

**Reverse Phase Analysis of SPA2 Reaction with SEQ. I.D. NO. 8****Figure 1**

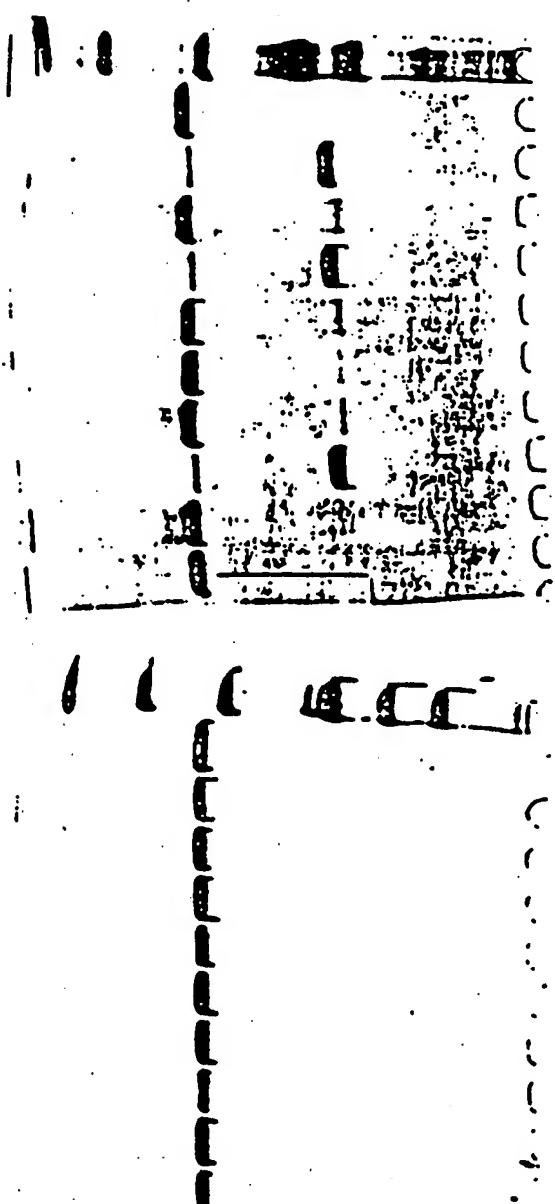
2/12

**Preparative Reverse Phase Analysis of PEG-Peptide (SEQ. I.D. No. 8) Dimer****Figure 2**

**Figure 3**



4/12



A. Non Reducing 10-20% SDS-PAGE, B. Reducing 10-20% SDS-PAGE

Lane	Seq. I.D. No.	8	16	18	13						
1	2	3	4	5	6	7	8	9	10	11	
MWM	EPP	Pep tide (μM)	400	400	400	400	400	400	400	400	...
EPP (μM)	22	22	22	22	22	22	22	22	22	22	22
DPLV's (mM)	1.1	0	1.1	0	1.1	0	1.1	0	1.1	0	1.1

Seq. I.D. No.	Sequence	IC <sub>50</sub> (μM)	EPOED <sub>50</sub> (μM)
8	GCTYSCHFGLPLTWCKPQQC	5	0.1
16	YSCHFGLPLTWCK	70	3
18	SCHFGLPLTWCK	90	IA
13	GCTYSCHFGLPLTWCKPQQ	8	0.08

Figure 4

5/12

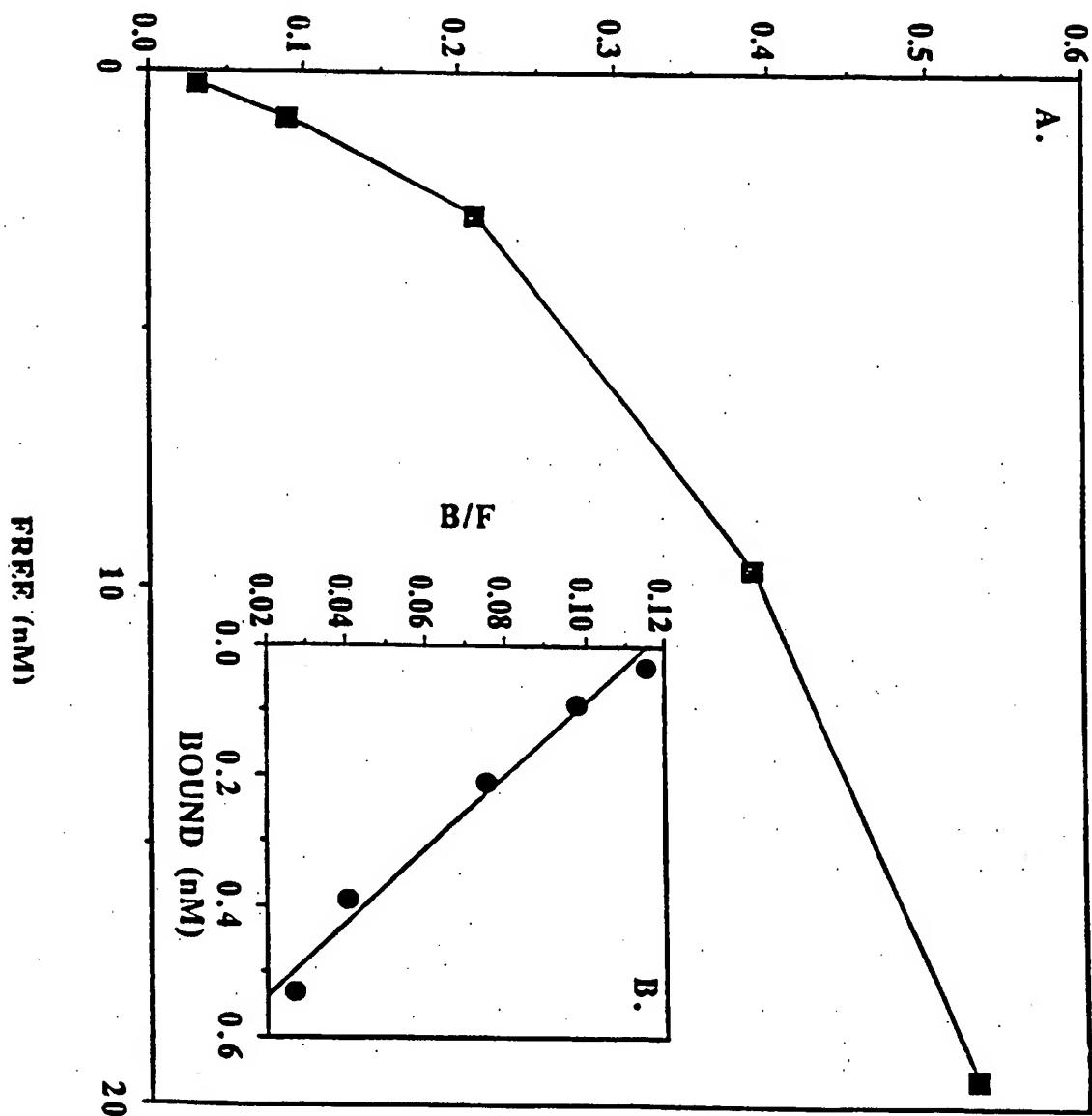
**BOUND (nM)**

Figure 5

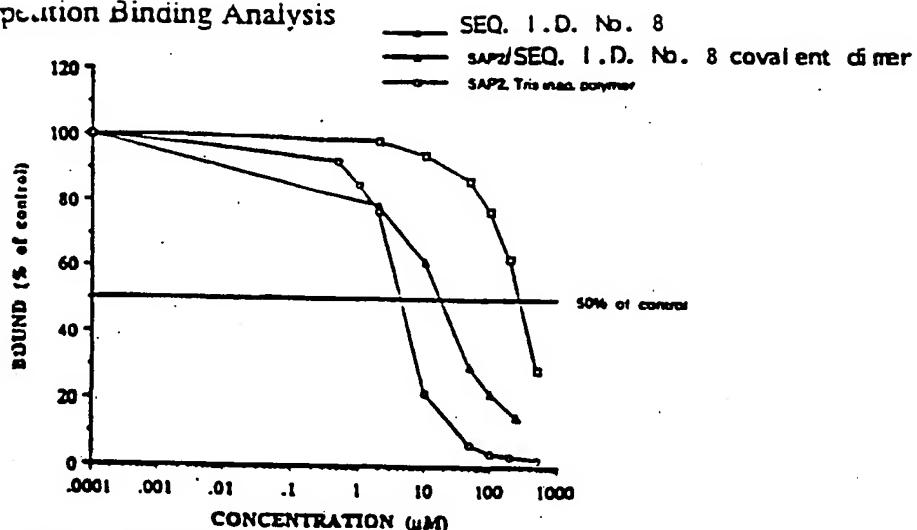
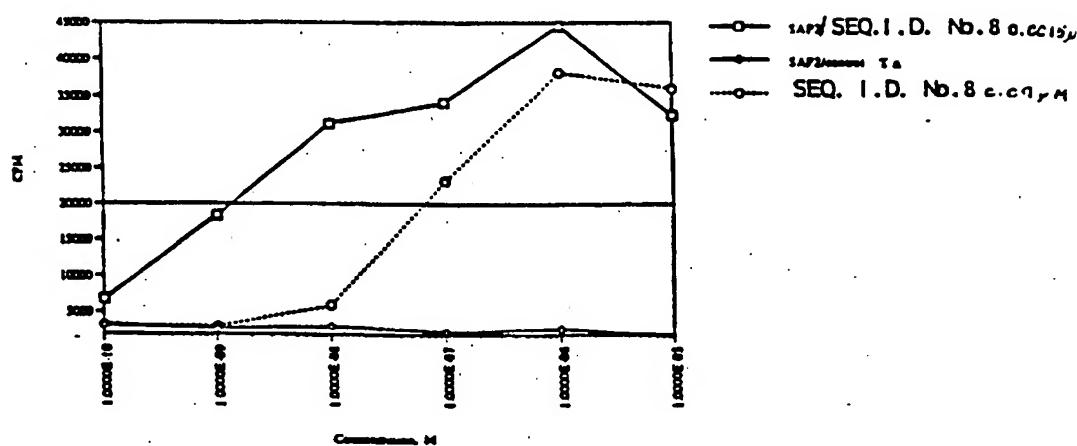
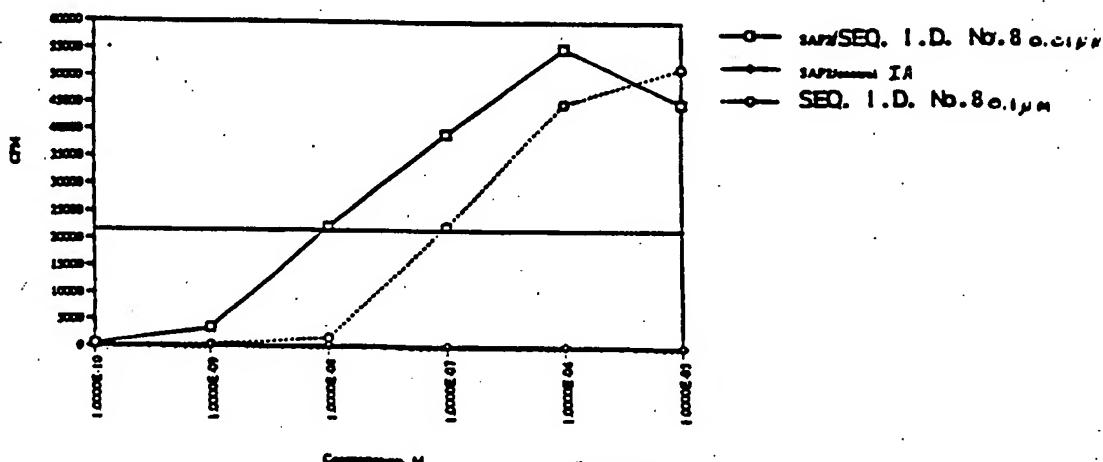
**A. [<sup>125</sup>I]EPO Competition Binding Analysis****B. Cell Proliferation, Human EPOR****C. Cell Proliferation, Murine EPOR**

Figure 6

7/12

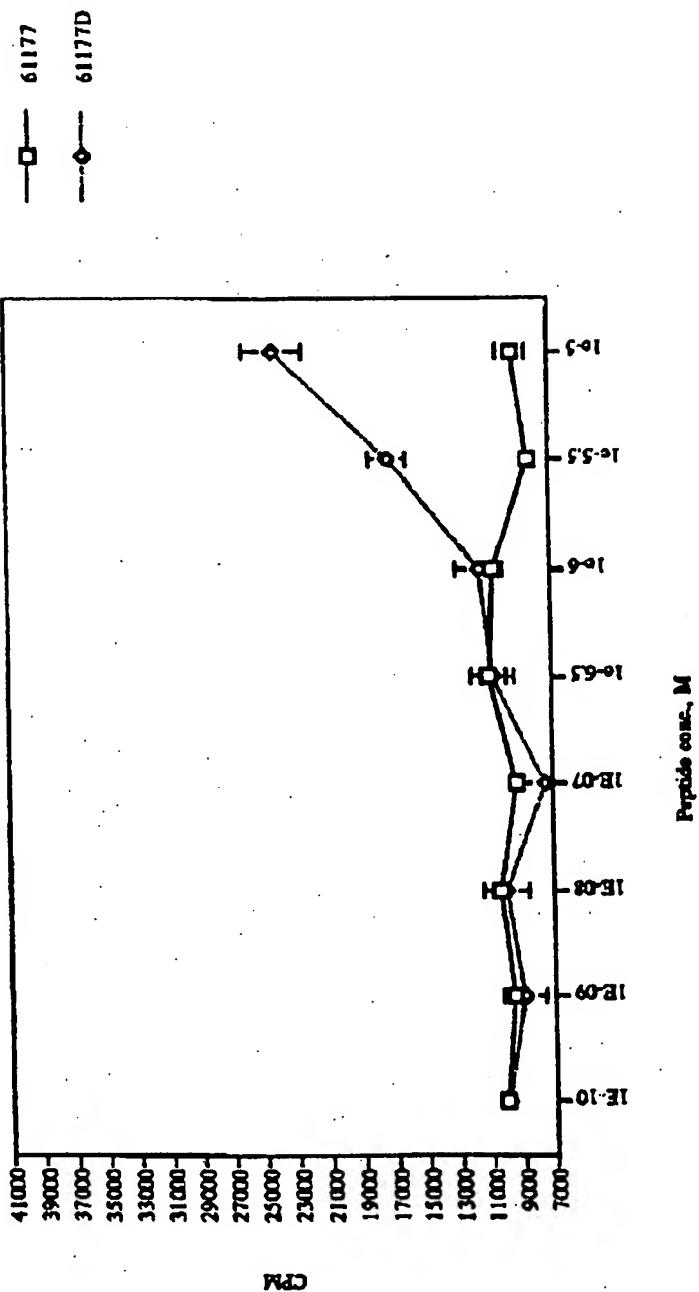


Figure 6  
Panel D

8/12

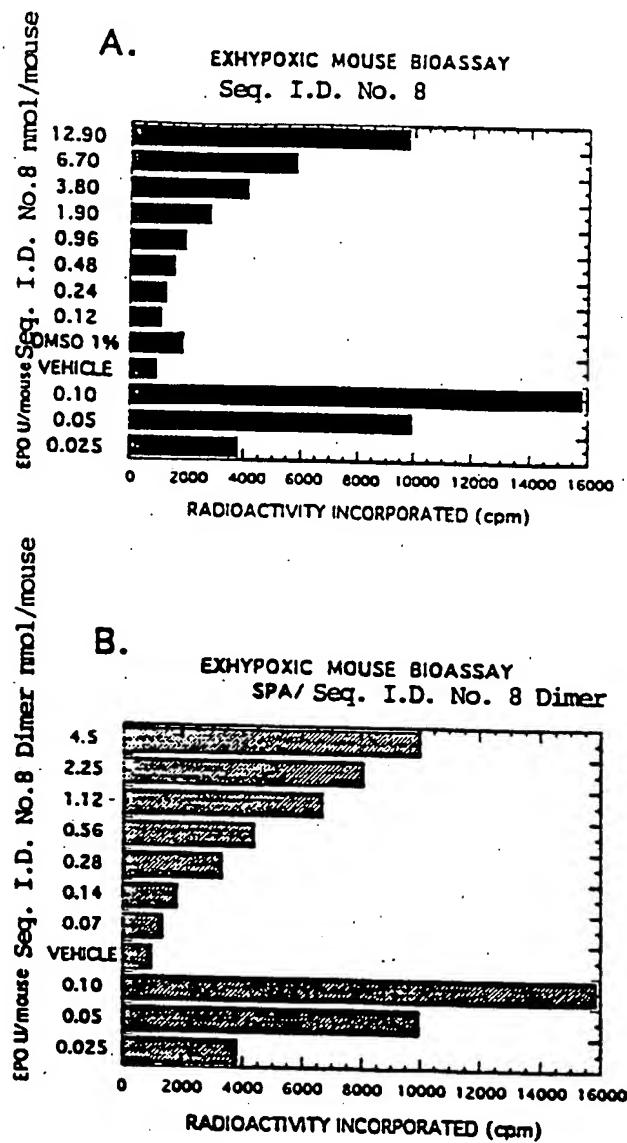


Figure 7

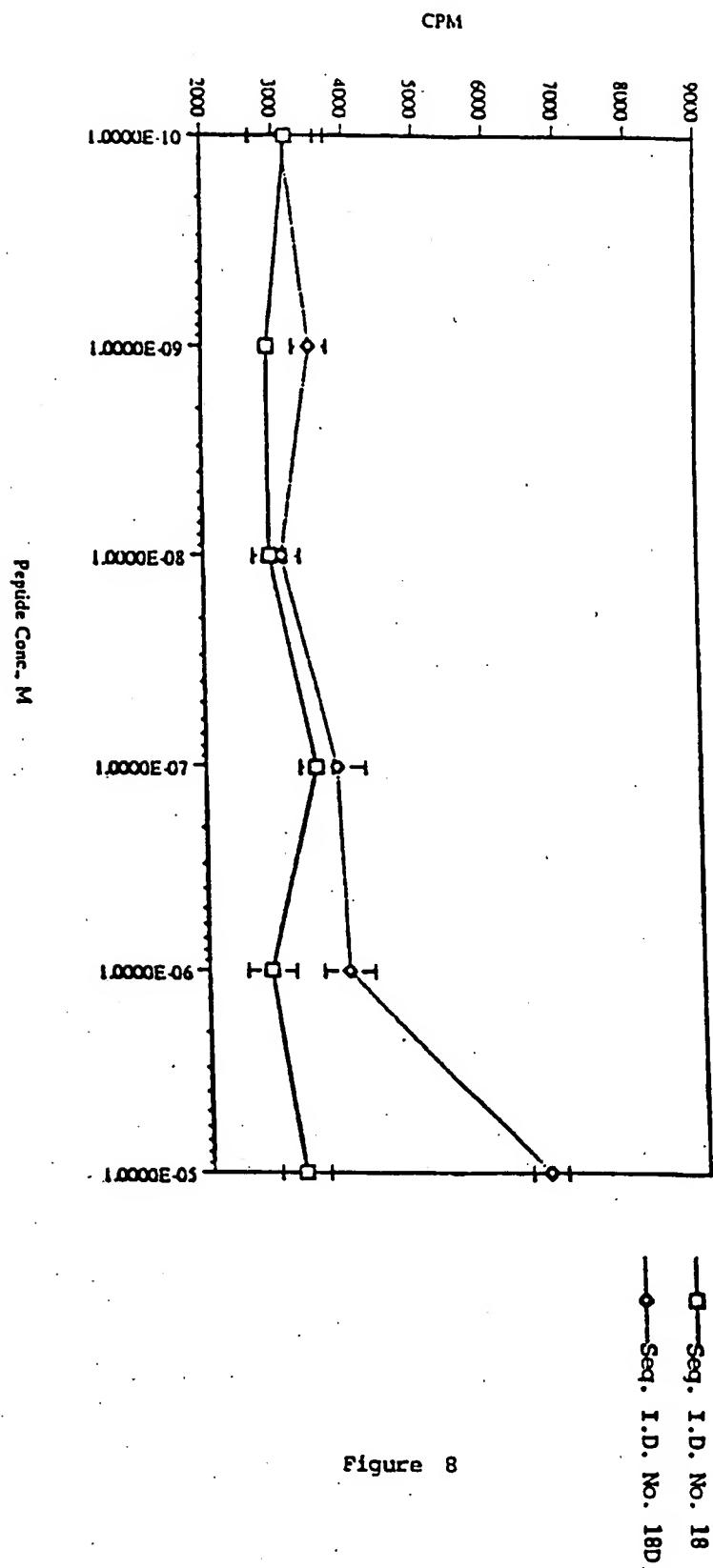


Figure 8

10/12

## FIGURE 9

Page 1 of 3

Ac-GGTYSCHFGPLTWVCKPQGG	SEQ ID NO: 20
GCTTACGCGPMTAVVCKPQGG	SEQ ID NO: 21
GATYSCFMGPMTAVVCKPQGG	SEQ ID NO: 22
GATYACPGPMTAVVCKPQGG	SEQ ID NO: 23
GATYSCFMGPMTAVVCKPQGG	SEQ ID NO: 24
GATYKCGMGPMTAVVCKPQGG	SEQ ID NO: 25
GATYTCMGPMTAVVCKPQGG	SEQ ID NO: 26
GATYLCRGPMTAVVCKPQGG	SEQ ID NO: 27
GATYVCPYGPITWCTPAGG	SEQ ID NO: 28
GATYDVCNGPITWCTPAGG	SEQ ID NO: 29
GATYLCFMGPTTWLCTAQRGGG	SEQ ID NO: 30
GATYLCFMGPATWVCGRYGG	SEQ ID NO: 31
GATYFCMGMGPATWVCGRYGG	SEQ ID NO: 32
GATYTCMGPMTAVVCTATRG	SEQ ID NO: 33
GATYVCFMGPMTAVVCTATRG	SEQ ID NO: 34
GATYSCFMGPMTAVVCTATRG	SEQ ID NO: 35
GATYLCFMGPTTWVCTYGG	SEQ ID NO: 36
GATYICRMGPMTAVVCTAAGG	SEQ ID NO: 37
GATYLCRGPATWVCGRMGG	SEQ ID NO: 38
GATYLCRGPVITWDCGYKGG	SEQ ID NO: 39
GATYSCPMGPITWVCTKAGG	SEQ ID NO: 40
GATYHCRMGPMTWVCRPVGG	SEQ ID NO: 41
GATYSCFGPLTWVCKPQGG	SEQ ID NO: 42
GATYXCLMGPPLTWVCTPQGG	SEQ ID NO: 43
GATYSCLMGPITWLCKPQGG	SEQ ID NO: 44
GATYHCRMGPPLTWVCTPQGG	SEQ ID NO: 45
GATYSCRMGPITWCTPPGG	SEQ ID NO: 46
GATYWCRMGPSTWECNAAGG	SEQ ID NO: 47
GATYLCFEGPITWVCAHYGG	SEQ ID NO: 48
GATYKCRLGPTIWVCSPLGG	SEQ ID NO: 49
GATYTCRGPETWVCRPNGG	SEQ ID NO: 50
GATYSCRMGPITWVCKPQGG	SEQ ID NO: 51
GATYTCRMGPITWVCLPAGG	SEQ ID NO: 52
GATYECFMGPMTWVCRPGGG	SEQ ID NO: 53

11/12

Figure 9  
Page 2 of 3

GGDYTCRNGPITWICTKAGG	SEQ ID NO: 54
GGVYSCRNGPTTNECRNPYVG	SEQ ID NO: 55
GGAYLCLRNGPITWVCRPQGG	SEQ ID NO: 56
GGEYSCRNGPNTWVCKPVGG	SEQ ID NO: 57
GGLYLCRNGPVTWECOPRGG	SEQ ID NO: 58
GGLYTCRNGPITAVCLLPGG	SEQ ID NO: 59
GGLYTCRNGPVTWVCTGAGG	SEQ ID NO: 60
GGVYKCRNGPLTNECRPTGG	SEQ ID NO: 61
GGDYNCRFGPLTWCCKPSGG	SEQ ID NO: 62
GGSYLCPFCFTTWLCSSACG	SEQ ID NO: 63
GGSYLCRNGPTTAVCTPMGG	SEQ ID NO: 64
GGSYLCRFGPTTWLCTQRGG	SEQ ID NO: 65
GGWVTCRNGPITWVCGVHGG	SEQ ID NO: 66
GGOLLCCIGPITWVCRWVGG	SEQ ID NO: 67
GGKYSFCMNGPTTAVCSPVGRGV	SEQ ID NO: 68
GGWVYCRIGPITWVCDTRIGG	SEQ ID NO: 69
GGHYYCRNGPMTWVCKKGAGG	SEQ ID NO: 70
GGTTQCHWIGPITHVCRARGG	SEQ ID NO: 71
GGPYHCRNGPITWVCGPVGG	SEQ ID NO: 72
GGEYRCRNGPISWVCSPOGGG	SEQ ID NO: 73
GGNYTCRFGPLTWECKTPQGGGA	SEQ ID NO: 74
GGSWDCRIGPITWVCKHSGG	SEQ ID NO: 75
VGNYTMCHFGPITWVCRPGGG	SEQ ID NO: 76
GGLYLCRNGPOTWVCKQPGGG	SEQ ID NO: 77
GGDYVCRNGPMTWVCAFYGR	SEQ ID NO: 78
GGWYSCLMGPMTWVCKAHRG	SEQ ID NO: 79
GGKYYCHWNGPMTWVCSFAGG	SEQ ID NO: 80
GGYVMCRIGPITWVCDIPGG	SEQ ID NO: 81
GSCLOCCIGPITWVCRHAGG	SEQ ID NO: 82
GGAYFZMFGPTTAVCTESGG	SEQ ID NO: 83
GGEYICRMGPLTWECKRTGG	SEQ ID NO: 84
GGLYACRMGPIWVCKYMAA	SEQ ID NO: 85
GGQYLCTFGPITWLCRGAGG	SEQ ID NO: 86
GGVYACRMGPIWVCSPLGG	SEQ ID NO: 87
GGYTTCRNGPITWVCSAHHGG	SEQ ID NO: 88
GGTYKCRNGPMTWVCRPVGG	SEQ ID NO: 89
GGNYYCRFGPITFECHPPTGG	SEQ ID NO: 90

12/12

Figure 9  
Page 3 of 3

GGEYLCAGGPHITWVCTSVGG	SEQ ID NO: 91
GGLYTCAGGPHITWVCLPAGG	SEQ ID NO: 92
GGLYTCAGGPHITWVCLPAGG	SEQ ID NO: 93